```
RESULT   1
HUMIHH
LOCUS       HUMIHH       1277 bp    mRNA            PRI       12-FEB-1995
DEFINITION  Homo sapiens indian hedgehog protein (IHH) mRNA, 5' end.
ACCESSION   L38517
VERSION     L38517.1  GI:663154
KEYWORDS    homologue; indian hedgehog protein.
SOURCE      Homo sapiens (clone HHH4) (tissue library: Clontech) fetus lung
            cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1277)
  AUTHORS   Marigo,V., Roberts,D.J., Lee,S.M.K., Tsukurov,O., Levi,T.,
            Gastier,J.M., Epstein,D.J., Gilbert,D.J., Martin,G.G.,
            Copeland,N.G., Seidman,C.E., Jenkins,N.A., Seidman,J.G.,
            McMahon,A.P. and Tabin,C.
  TITLE     Cloning, expression and chromosomal location of SHH and IHH, two
            human homologues of the Drosophila segment polarity gene Hedgehog
  JOURNAL   Unpublished (1995)
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ORIGIN
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Matches 1272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    411 CAGTGGCCCGGTGTGAAGCTGCGGGTGACCGAGGGCTGGGACGAGGACGGCCACCACTCA 470
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Db    425 AGCGATGTGCTCATTTTCCTGGACCGCGAGCCCCACAGGCTGAGAGCCTTCCAGGTCATC 484

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Qy    891 GACAATCACACGGAGCCGGCAGCCCGCTTCCGGGCCACATTTGCCAGCCACGTGCAGCCT 950
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RESULT 2

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: June 5, 2000, 04:52:15 ; Search time 1833.88 Seconds
(without alignments)
-860.399 Million cell updates/sec

Title: US-08-900-220-7
Perfect score: 1622
Sequence: 1 CATCAGCCCACCAGGAGACC.....CATTGGGAGGGCCCATTCCC 1622

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 882769 seqs, -486395729 residues

Total number of hits satisfying chosen parameters: 1765538

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : GenEmbl:*
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2: gb_ba2:*
3: gb_om:*
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58: gb_htg14:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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3	1114.8	68.7	2103	12	MMU85610	U85610 Mus musculu
4	936	57.7	939	5	AR063086	AR063086 Sequence
5	869.4	53.6	173557	43	AC016762	AC016762 Homo sapi
6	843.2	52.0	1056	5	AR021200	AR021200 Sequence
7	843.2	52.0	1056	5	AR063082	AR063082 Sequence
8	828.6	51.1	1011	12	MMIHH	X76291 M.musculus
9	757.4	46.7	1958	4	GGU58511	U58511 Gallus gall
10	661.2	40.8	683	9	AB010092S3	AB018076 Homo sapi
11	618.8	38.2	1635	4	AF047466	AF047466 Notophtha
12	509.6	31.4	1230	4	XLU26404	U26404 Xenopus lae
13	461.4	28.4	1567	4	CHKZPAMED	L28099 Gallus gall
14	459	28.3	1277	5	AR021198	AR021198 Sequence
15	459	28.3	1277	5	AR063080	AR063080 Sequence
16	453.8	28.0	1425	5	AR063085	AR063085 Sequence
17	453.8	28.0	1576	9	HUMSHH	L38518 Homo sapien
18	440.4	27.2	1314	12	MMSHH	X76290 M.musculus
19	439.2	27.1	533	12	AF162914	AF162914 Rattus no
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22	436.6	26.9	1807	4	NEWSPA	D63339 Cynops pyrr
23	436.2	26.9	1718	4	AB029748	AB029748 Paralicht
24	432.2	26.6	1549	4	AF003532	AF003532 Pleurodel
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26	419.8	25.9	1190	5	AR021199	AR021199 Sequence
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33	418.2	25.8	2600	4	ZEFVHH1A	L27585 Brachydanio
34	416.6	25.7	1257	4	DRU30711	U30711 Danio rerio
35	402.2	24.8	2447	4	XELXSH	L39213 Xenopus lae
36	400.6	24.7	1335	4	XLU26314	U26314 Xenopus lae
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ALIGNMENTS

```
RESULT   1
HUMIHH
LOCUS       HUMIHH       1277 bp    mRNA            PRI       12-FEB-1995
DEFINITION  Homo sapiens indian hedgehog protein (IHH) mRNA, 5' end.
ACCESSION   L38517
VERSION     L38517.1  GI:663154
KEYWORDS    homologue; indian hedgehog protein.
SOURCE      Homo sapiens (clone HHH4) (tissue library: Clontech) fetus lung
            cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1277)
  AUTHORS   Marigo,V., Roberts,D.J., Lee,S.M.K., Tsukurov,O., Levi,T.,
            Gastier,J.M., Epstein,D.J., Gilbert,D.J., Martin,G.G.,
            Copeland,N.G., Seidman,C.E., Jenkins,N.A., Seidman,J.G.,
            McMahon,A.P. and Tabin,C.
  TITLE     Cloning, expression and chromosomal location of SHH and IHH, two
            human homologues of the Drosophila segment polarity gene Hedgehog
  JOURNAL   Unpublished (1995)
FEATURES             Location/Qualifiers
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BASE COUNT      217 a    418 c    407 g    235 t
ORIGIN
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  Query Match             78.4%;  Score 1272;  DB 9;  Length 1277;
  Best Local Similarity   100.0%;  Pred. No. 6e-211;
  Matches 1272;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     411 CAGTGGCCCGGTGTGAAGCTGCGGGTGACCGAGGGCTGGGACGAGGACGGCCACCACTCA 470
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Qy    1551 CGACTCCCAACTCAGCCTGCTCTCACTACGAGTTTTCATACTCTGCCTCCCCCATTGGGA 1610
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1205 CGACTCCCAACTCAGCCTGCTCTCACTACGAGTTTTCATACTCTGCCTCCCCCATTGGGA 1264

Qy    1611 GGGCCCATTCCC 1622
           ||||||||||||
Db    1265 GGGCCCATTCCC 1276
```

RESULT 2

```
G28584
LOCUS       G28584       1277 bp    DNA             STS       11-JUL-1996
DEFINITION  human STS SHGC-35345, sequence tagged site.
ACCESSION   G28584
VERSION     G28584.1  GI:1408399
KEYWORDS    STS; STS sequence; primer; sequence tagged site.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1277)
  AUTHORS   Myers,R.M.
  JOURNAL   Unpublished (1996)
COMMENT
            Contact: Richard M. Myers
            Stanford Human Genome Center (SHGC)
            Stanford University School of Medicine
            Department of Genetics, M-344, Stanford, CA 94305, USA
            Tel: 4157259687
            Fax: 4157259689
            Email: myers@shgc.stanford.edu

            Primer A: GGGTCCAGAAGCCTCTCAG
            Primer B: CTCAAGGTCTCTAGGAGAGAGGG
            STS size: 217
            PCR Profile:
                    Initial incubation: 94 degrees C for 90 seconds

                    Denaturation:       94 degrees C for 15 seconds
                    Annealing:          62 degrees C for 23 seconds
                    Polymerization:     72 degrees C for 30 seconds
                    PCR Cycles:         30
                    Thermal Cycler:     Perkin Elmer 9600
            Protocol:
                    Template:       25 ng
                    Primer:         each 1 uM
                    dNTPs:          each 200 uM
                    Taq Polymerase: 0.05 units/ul
                    Total Vol:      10 ul

            Buffer:
                    MgCl2:          2.5 mM
                    KCl:            50  mM
                    Tris-HCl:       20  mM
                    pH:             8.3

            Prepared with primer pairs provided by Sandoz, derived from L38517
            -- Washington University/Merck EST sequence.
FEATURES             Location/Qualifiers
     source          1. .1277
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="2"
     STS             978. .1194
     primer_bind     978. .996
     primer_bind     complement(1172. .1194)
BASE COUNT      217 a    418 c    407 g    235 t
ORIGIN
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Query Match 78.4%; Score 1272; DB 13; Length 1277;
Best Local Similarity 100.0%; Pred. No. 6e-211;
Matches 1272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    351 CGCCTCATGACCCAGCGCTGCAAGGACCGCCTGAACTCGCTGGCTATCTCGGTGATGAAC 410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5 CGCCTCATGACCCAGCGCTGCAAGGACCGCCTGAACTCGCTGGCTATCTCGGTGATGAAC 64

Qy    411 CAGTGGCCCGGTGTGAAGCTGCGGGTGACCGAGGGCTGGGACGAGGACGGCCACCACTCA 470
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     65 CAGTGGCCCGGTGTGAAGCTGCGGGTGACCGAGGGCTGGGACGAGGACGGCCACCACTCA 124

Qy    471 GAGGAGTCCCTGCATTATGAGGGCCGCGCGGTGGACATCACCACATCAGACCGCGACCGC 530
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    125 GAGGAGTCCCTGCATTATGAGGGCCGCGCGGTGGACATCACCACATCAGACCGCGACCGC 184

Qy    531 AATAAGTATGGACTGCTGGCGCGCTTGGCAGTGGAGGCCGGCTTTGACTGGGTGTATTAC 590
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    185 AATAAGTATGGACTGCTGGCGCGCTTGGCAGTGGAGGCCGGCTTTGACTGGGTGTATTAC 244

Qy    591 GAGTCAAAGGCCCACGTGCATTGCTCCGTCAAGTCCGAGCACTCGGCCGCAGCCAAGACG 650
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    245 GAGTCAAAGGCCCACGTGCATTGCTCCGTCAAGTCCGAGCACTCGGCCGCAGCCAAGACG 304

Qy    651 GGCGGCTGCTTCCCTGCCGGAGCCCAGGTACGCCTGGAGAGTGGGGCGCGTGTGGCCTTG 710
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    305 GGCGGCTGCTTCCCTGCCGGAGCCCAGGTACGCCTGGAGAGTGGGGCGCGTGTGGCCTTG 364

Qy    711 TCAGCCGTGAGGCCGGGAGACCGTGTGCTGGCCATGGGGGAGGATGGGAGCCCCACCTTC 770
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    365 TCAGCCGTGAGGCCGGGAGACCGTGTGCTGGCCATGGGGGAGGATGGGAGCCCCACCTTC 424

Qy    771 AGCGATGTGCTCATTTTCCTGGACCGCGAGCCCCACAGGCTGAGAGCCTTCCAGGTCATC 830
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    425 AGCGATGTGCTCATTTTCCTGGACCGCGAGCCCCACAGGCTGAGAGCCTTCCAGGTCATC 484

Qy    831 GAGACTCAGGACCCCCCACGCCGCCTGGCACTCACACCCGCTCACCTGCTCTTTACGGCT 890
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Db    485 GAGACTCAGGACCCCCCACGCCGCCTGGCACTCACACCCGCTCACCTGCTCTTTACGGCT 544

Qy    891 GACAATCACACGGAGCCGGCAGCCCGCTTCCGGGCCACATTTGCCAGCCACGTGCAGCCT 950
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Db    545 GACAATCACACGGAGCCGGCAGCCCGCTTCCGGGCCACATTTGCCAGCCACGTGCAGCCT 604

Qy    951 GGCCAGTACGTGCTGGTGGCTGGGGTGCCAGGCCTGCAGCCTGCCCGCGTGGCAGCTGTC 1010
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    605 GGCCAGTACGTGCTGGTGGCTGGGGTGCCAGGCCTGCAGCCTGCCCGCGTGGCAGCTGTC 664

Qy   1011 TCTACACACGTGGCCCTCGGGGCCTACGCCCCGCTCACAAAGCATGGGACACTGGTGGTG 1070
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    665 TCTACACACGTGGCCCTCGGGGCCTACGCCCCGCTCACAAAGCATGGGACACTGGTGGTG 724

Qy   1071 GAGGATGTGGTGGCATCCTGCTTCGCGGCCGTGGCTGACCACCACCTGGCTCAGTTGGCC 1130
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    725 GAGGATGTGGTGGCATCCTGCTTCGCGGCCGTGGCTGACCACCACCTGGCTCAGTTGGCC 784

Qy   1131 TTCTGGCCCCTGAGACTCTTTCACAGCTTGGCATGGGGCAGCTGGACCCCGGGGGAGGGT 1190
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    785 TTCTGGCCCCTGAGACTCTTTCACAGCTTGGCATGGGGCAGCTGGACCCCGGGGGAGGGT 844

Qy   1191 GTGCATTGGTACCCCCAGCTGCTCTACCGCCTGGGGCGTCTCCTGCTAGAAGAGGGCAGC 1250
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    845 GTGCATTGGTACCCCCAGCTGCTCTACCGCCTGGGGCGTCTCCTGCTAGAAGAGGGCAGC 904

Qy   1251 TTCCACCCACTGGGCATGTCCGGGGCAGGGAGCTGAAAGGACTCCACCGCTGCCCTCCTG 1310
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    905 TTCCACCCACTGGGCATGTCCGGGGCAGGGAGCTGAAAGGACTCCACCGCTGCCCTCCTG 964

Qy   1311 GAACTGCTGTACTGGGTCCAGAAGCCTCTCAGCCAGGAGGGAGCTGGCCCTGGAAGGGAC 1370
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    965 GAACTGCTGTACTGGGTCCAGAAGCCTCTCAGCCAGGAGGGAGCTGGCCCTGGAAGGGAC 1024

Qy   1371 CTGAGCTGGGGGACACTGGCTCCTGCCATCTCCTCTGCCATGAAGATACACCATTGAGAC 1430
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1025 CTGAGCTGGGGGACACTGGCTCCTGCCATCTCCTCTGCCATGAAGATACACCATTGAGAC 1084

Qy   1431 TTGACTGGGCAACACCAGCGTCCCCCACCCGCGTCGTGGTGTAGTCATAGAGCTGCAAGC 1490
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1085 TTGACTGGGCAACACCAGCGTCCCCCACCCGCGTCGTGGTGTAGTCATAGAGCTGCAAGC 1144

Qy   1491 TGAGCTGGCGAGGGGATGGTTGTTGACCCCTCTCTCCTAGAGACCTTGAGGCTGGCACGG 1550
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Db   1145 TGAGCTGGCGAGGGGATGGTTGTTGACCCCTCTCTCCTAGAGACCTTGAGGCTGGCACGG 1204

Qy   1551 CGACTCCCAACTCAGCCTGCTCTCACTACGAGTTTTCATACTCTGCCTCCCCCATTGGGA 1610
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Db   1205 CGACTCCCAACTCAGCCTGCTCTCACTACGAGTTTTCATACTCTGCCTCCCCCATTGGGA 1264

Qy   1611 GGGCCCATTCCC 1622
          ||||||||||||
Db   1265 GGGCCCATTCCC 1276


RESULT   3
MMU85610
LOCUS       MMU85610     2103 bp    mRNA            ROD       16-MAR-1997
DEFINITION  Mus musculus Indian hedgehog protein (Ihh) mRNA, complete cds.
ACCESSION   U85610
VERSION     U85610.1  GI:1890096
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2103)
  AUTHORS   Valentini,R.P., Brookhiser,W.T., Park,J., Yang,T., Briggs,J.,
            Dressler,G. and Holzman,L.B.
  TITLE     Post-translational Processing and Renal Expression of Mouse Indian
            Hedgehog
  JOURNAL   J. Biol. Chem. (1997) In press
REFERENCE   2  (bases 1 to 2103)
  AUTHORS   Valentini,R.P., Brookhiser,W.T., Park,J., Yang,T., Briggs,J.,
            Dressler,G. and Holzman,L.B.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-1997) Internal Medicine/Division of Nephrology,
            University of Michigan Medical School, 1560 MSRB II--Box 0676, Ann
            Arbor, MI 48109-0676, USA
FEATURES             Location/Qualifiers
     source          1. .2103
                     /organism="Mus musculus"
                     /strain="CD-1"
                     /db_xref="taxon:10090"
     gene            184. .1533
                     /gene="Ihh"
     CDS             184. .1533
                     /gene="Ihh"
                     /codon_start=1
                     /product="Indian hedgehog protein"
                     /protein_id="AAB49692.1"
                     /db_xref="GI:1890097"
                     /translation="MESPRATQTPESPKLSQPRAHLSAHQAPSPAALPGYPAMSPAWL
                     RPRLRFCLFLLLLLLVPAARGCGPGRVVGSRRRPPRKLVPLAYKQFSPNVPEKTLGAS
                     GRYEGKIARSSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQW
                     PGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWVYY
                     ESKAHVHCSVKSEHSAAAKTGGCFPAGAQVRLENGERVALSAVKPGDRVLAMGEDGTP
                     TFSDVLIFLDREPNRLRAFQVIETQDPPRRLALTPAHLLFIADNHTEPAAHFRATFAS
                     HVQPGQYVLVSGVPGLQPARVAAVSTHVALGSYAPLTRHGTLVVEDVVASCFAAVADH
                     HLAQLAFWPLRLFPSLAWGSWTPSEGVHWYPQMLYRLGRLLLEESTFHPLGMSGAGS"
BASE COUNT      376 a    684 c    628 g    415 t
ORIGIN


  Query Match           68.7%;  Score 1114.8;  DB 12;  Length 2103;
  Best Local Similarity  85.5%;  Pred. No. 8e-184;
  Matches 1293;  Conservative    0;  Mismatches  202;  Indels   17;  Gaps    4;

Qy      2 ATCAGCCCACCAGGAGACCTCGCCCGCCGCTCCCCCGGGCTCCCCGGCCATGTCTCCCGC 61
          |||||||||||| | |||||||||| |||| |||||||| ||||||||||||||||||
Db    249 ATCAGCCCACCAGGCGCCCTCGCCCGCTGCTCTCCCGGGCTACCCGGCCATGTCTCCCGC 308

Qy     62 CCGGCTCCGGCCCCGACTGCACTTCTGCCTGGTCCTGTTGCTGCTGCTGGTGGTGCCCGC 121
          | ||||||||||||||||||  ||||| ||| ||||| ||||||||||  |||||||||
Db    309 CTGGCTCCGGCCCCGACTGCGGTTCTGTCTGTTCCTGCTGCTGCTGCTTCTGGTGCCGGC 368

Qy    122 GGCATGGGGCTGCGGGCCGGGTCGGGTGGTGGGCAGCCGCCGGCGACCGCCACGCAAACT 181
          |||  |||||||||||||||| ||||||||||||||||||||| | ||||| |||||||||
Db    369 GGCGCGGGGCTGCGGGCCGGGCCGGGTGGTGGGCAGCCGCCGGAGGCCGCCTCGCAAGCT 428

Qy    182 CGTGCCGCTCGCCTACAAGCAGTTCAGCCCCAATGTGCCCGAGAAGACCCTGGGCGCCAG 241
          |||||| || |||||||||||||||||||||| ||||| ||||||||||||||||||||
Db    429 CGTGCCTCTTGCCTACAAGCAGTTCAGCCCCAACGTGCCGGAGAAGACCCTGGGCGCCAG 488

Qy    242 CGGACGCTATGAAGGCAAGATCGCTCGCAGCTCCGAGCGCTTCAAGGAGCTCACCCCCAA 301
          ||| ||||| |||||||||||||| |||||||| |||||||||| ||||||||||||||
Db    489 CGGGCGCTACGAAGGCAAGATCGCGCGCAGCTCTGAGCGCTTCAAAGAGCTCACCCCCAA 548

Qy    302 TTACAATCCAGACATCATCTTCAAGGACGAGGAGAACACAGGCGCCGACCGCCTCATGAC 361
          |||||||| |||||||||||||||||||||||||||||||| || ||||||||||||||||
Db    549 CTACAATCCCGACATCATCTTCAAGGACGAGGAGAACACGGGTGCCGACCGCCTCATGAC 608

Qy    362 CCAGCGCTGCAAGGACCGCCTGAACTCGCTGGCTATCTCGGTGATGAACCAGTGGCCCGG 421
          |||||||||||||||||| |||||||| ||||| ||||| || ||||||||||||||| ||
Db    609 CCAGCGCTGCAAGGACCGTCTGAACTCACTGGCCATCTCTGTCATGAACCAGTGGCCTGG 668

Qy    422 TGTGAAGCTGCGGGTGACCGAGGGCTGGGACGAGGACGGCCACCACTCAGAGGAGTCCCT 481
          ||||||| |||||||||||||| |||||||| || || ||||| ||||||||||||||  |
Db    669 TGTGAAACTGCGGGTGACCGAAGGCTGGGATGAAGATGGCCATCACTCAGAGGAGTCTTT 728

Qy    482 GCATTATGAGGGCCGCGCGGTGGACATCACCACATCAGACCGCGACCGCAATAAGTATGG 541
          || |||||||||||||||||||| |||||||| |||||||| ||||| ||||||||||||
Db    729 ACACTATGAGGGCCGCGCGGTGGATATCACCACCTCAGACCGTGACCGAAATAAGTATGG 788

Qy    542 ACTGCTGGCGCGCTTGGCAGTGGAGGCCGGCTTTGACTGGGTGTATTACGAGTCAAAGGC 601
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Db    789 ACTGCTGGCGCGCTTAGCAGTGGAGGCCGGCTTCGACTGGGTGTATTACGAGTCCAAGGC 848

Qy    602 CCACGTGCATTGCTCCGTCAAGTCCGAGCACTCGGCCGCAGCCAAGACGGGCGGCTGCTT 661
          |||||||||||||||| |||||||| ||||| ||||||| |||||||| || ||||||||
Db    849 CCACGTGCATTGCTCTGTCAAGTCTGAGCATTCGGCCGCTGCCAAGACAGGTGGCTGCTT 908

Qy    662 CCCTGCCGGAGCCCAGGTACGCCTGGAGAGTGGGGCGCGTGTGGCCTTGTCAGCCGTGAG 721
          |||||||||||||||||| |||| |||| |||||||||| ||||||| || |
Db    909 TCCTGCCGGAGCCCAGGTGCGCCTAGAGAACGGGGAGCGTGTGGCCCTGTCAGCTGTAAA 968

Qy    722 GCCGGGAGACCGTGTGCTGGCCATGGGGGAGGATGGGAGCCCCACCTTCAGCGATGTGCT 781
          ||| |||||||| |||||||||||||||||||||||| |||||||||| ||||||||
Db    969 GCCAGGAGACCGGGTGCTGGCCATGGGGGAGGATGGGACCCCCACCTTCAGTGATGTGCT 1028

Qy    782 CATTTTCCTGGACCGCGAGCCCCACAGGCTGAGAGCCTTCCAGGTCATCGAGACTCAGGA 841
          ||||||||||||||||||  || |||||||||| ||||||||||||||||||||||||||
Db   1029 TATTTTCCTGGACCGCGAGCCAAACCGGCTGAGAGCTTTCCAGGTCATCGAGACTCAGGA 1088

Qy    842 CCCCCCACGCCGCCTGGCACTCACACCCGCTCACCTGCTCTTTACGGCTGACAATCACAC 901
          || || || |||| |||| || || |||||||||| |  || |||||||| ||
Db   1089 TCCTCCGCGTCGGCTGGCGCTCACGCCTGCCCACCTGCTCTTCATTGCGGACAATCATAC 1148

Qy    902 GGAGCCGGCAGCCCGCTTCCGGGCCACATTTGCCAGCCACGTGCAGCCTGGCCAGTACGT 961
          || || ||||||| |||||||||||||||||||||||| ||||| || ||||| || ||
Db   1149 AGAACCAGCAGCCCACTTCCGGGCCACATTTGCCAGCCATGTGCAACCAGGCCAATATGT 1208

Qy    962 GCTGGTGGCTGGGGTGCCAGGCCTGCAGCCTGCCCGCGTGGCAGCTGTCTCTACACACGT 1021
          ||||||  | |||| |||||||| |||||||| || |||||||||||||| || |||||
Db   1209 GCTGGTATCAGGGGTACCAGGCCTCCAGCCTGCTCGGGTGGCAGCTGTCTCCACCCACGT 1268

Qy    1022 GGCCCTCGGGGCCTACGCCCCGCTCACAAAGCATGGGACACTGGTGGTGGAGGATGTGGT 1081
           |||||| ||| |||| || || ||||||| |||||||||||| ||||||||||||||||
Db    1269 GGCCCTTGGGTCCTATGCTCCTCTCACAAGGCATGGGACACTTGTGGTGGAGGATGTGGT 1328

Qy    1082 GGCATCCTGCTTCGCGGCCGTGGCTGACCACCACCTGGCTCAGTTGGCCTTCTGGCCCCT 1141
           ||| |||||||| || || |||||||||||||| |||||||||||||||||||||||||
Db    1329 GGCCTCCTGCTTTGCAGCTGTGGCTGACCACCATCTGGCTCAGTTGGCCTTCTGGCCCCT 1388

Qy    1142 GAGACTCTTTCACAGCTTGGCATGGGGCAGCTGGACCCCGGGGGAGGGGTGTGCATTGGTA 1201
           | |||| |||| ||| |||||||||||||||||||||  | |||||||| || |||||
Db    1389 GCGACTGTTTCCCAGTTTGGCATGGGGCAGCTGGACCCCAAGTGAGGGTGTTCACTGGTA 1448

Qy    1202 CCCCCAGCTGCTCTACCGCCTGGGGCGTCTCCTGCTAGAAGAGGGCAGCTTCCACCCACT 1261
           ||| ||| |||||||||||||||||||||||| |||||||||| ||| |||||| |||||
Db    1449 CCCTCAGATGCTCTACCGCCTGGGGCGTCTCTTGCTAGAAGAGAGCACCTTCCATCCACT 1508

Qy    1262 GGGCATGTCCGGGGCAGGGAGCTGAAAGGACTC-CACCGCTGCCCTCCTGGAACTGCTGT 1320
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Db   1509 GGGCATGTCTGGGGCAGGAAGCTGAAGGGACTCTAACCACTGCCCTCCTGGAACTGCTGT 1568

Qy   1321 ACTGGGTCCAGAAGCCTCTCAGCCAGGAGGGAGCTGGCCCTGGAAGGGACCTGAGCTGGG 1380

Db   1569 GCTGGATCCAAAGGCCTCCTCACCAGGAAGGCTCTGGCCCTGGAAGGCACCTGGCCTGAG 1628

Qy   1381 GGACACTGGCTCCTGCCATCTCCTCTGCCATGAAGATACACCATTGAGACTTGACTGGGC 1440

Db   1629 GTTGTCTCCGTC-------CTCTGTGCCAGAGTGGAGACACCATTGAGACTTGACCAGG- 1681

Qy   1441 AACACCAGCGTCCCCCACCCGCGTCGTGGTGTAGTCATAGAGCTGCAAGCTGAGCTGGCG 1500

Db   1681 --TTGCTGGGCCCCGAACCTTCATCTTGGTG------TAGAGCTGTGAACTGAGCTGACA 1732

Qy   1501 AGGGGATGGTTG 1512

Db   1733 AGCGTGTGGTAG 1744


RESULT   4
AR063086
LOCUS       AR063086      939 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 7 from patent US 5844079.
ACCESSION   AR063086
VERSION     AR063086.1  GI:5990777
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 939)
  AUTHORS   Ingham,P.W., McMahon,A.P. and Tabin,C.J.
  TITLE     Vertebrate embryonic pattern-inducing proteins, and uses related
            thereto
  JOURNAL   Patent: US 5844079-A 7 01-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .939
                     /organism="unknown"
BASE COUNT      154 a    305 c    314 g    166 t
ORIGIN


  Query Match           57.7%;  Score 936;  DB 5;  Length 939;
  Best Local Similarity  100.0%;  Pred. No. 8e-153;
  Matches  936;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    351 CGCCTCATGACCCAGCGCTGCAAGGACCGCCTGAACTCGCTGGCTATCTCGGTGATGAAC 410

Db      4 CGCCTCATGACCCAGCGCTGCAAGGACCGCCTGAACTCGCTGGCTATCTCGGTGATGAAC 63

Qy    411 CAGTGGCCCGGTGTGAAGCTGCGGGTGACCGAGGGCTGGGACGAGGACGGCCACCACTCA 470

Db     64 CAGTGGCCCGGTGTGAAGCTGCGGGTGACCGAGGGCTGGGACGAGGACGGCCACCACTCA 123

Qy    471 GAGGAGTCCCTGCATTATGAGGGCCGCGCGGTGGACATCACCACATCAGACCGCGACCGC 530

Db    124 GAGGAGTCCCTGCATTATGAGGGCCGCGCGGTGGACATCACCACATCAGACCGCGACCGC 183

Qy    531 AATAAGTATGGACTGCTGGCGCGCTTGGCAGTGGAGGCCGGCTTTGACTGGGTGTATTAC 590

Db    184 AATAAGTATGGACTGCTGGCGCGCTTGGCAGTGGAGGCCGGCTTTGACTGGGTGTATTAC 243

Qy    591 GAGTCAAAGGCCCACGTGCATTGCTCCGTCAAGTCCGAGCACTCGGCCGCAGCCAAGACG 650

Db    244 GAGTCAAAGGCCCACGTGCATTGCTCCGTCAAGTCCGAGCACTCGGCCGCAGCCAAGACG 303

Qy    651 GGCGGCTGCTTCCCTGCCGGAGCCCAGGTACGCCTGGAGAGTGGGGCGCGTGTGGCCTTG 710

Db    304 GGCGGCTGCTTCCCTGCCGGAGCCCAGGTACGCCTGGAGAGTGGGGCGCGTGTGGCCTTG 363

Qy    711 TCAGCCGTGAGGCCGGGAGACCGTGTGCTGGCCATGGGGGAGGATGGGAGCCCCACCTTC 770

Db    364 TCAGCCGTGAGGCCGGGAGACCGTGTGCTGGCCATGGGGGAGGATGGGAGCCCCACCTTC 423

Qy    771 AGCGATGTGCTCATTTTCCTGGACCGCGAGCCCCACAGGCTGAGAGCCTTCCAGGTCATC 830

Db    424 AGCGATGTGCTCATTTTCCTGGACCGCGAGCCCCACAGGCTGAGAGCCTTCCAGGTCATC 483

Qy    831 GAGACTCAGGACCCCCCACGCCGCCTGGCACTCACACCCGCTCACCTGCTCTTTACGGCT 890

Db    484 GAGACTCAGGACCCCCCACGCCGCCTGGCACTCACACCCGCTCACCTGCTCTTTACGGCT 543

Qy    891 GACAATCACACGGAGCCGGCAGCCCGCTTCCGGGCCACATTTGCCAGCCACGTGCAGCCT 950

Db    544 GACAATCACACGGAGCCGGCAGCCCGCTTCCGGGCCACATTTGCCAGCCACGTGCAGCCT 603

Qy    951 GGCCAGTACGTGCTGGTGGCTGGGGTGCCAGGCCTGCAGCCTGCCCGCGTGGCAGCTGTC 1010

Db    604 GGCCAGTACGTGCTGGTGGCTGGGGTGCCAGGCCTGCAGCCTGCCCGCGTGGCAGCTGTC 663

Qy   1011 TCTACACACGTGGCCCTCGGGGCCTACGCCCCGCTCACAAAGCATGGGACACTGGTGGTG 1070

Db    664 TCTACACACGTGGCCCTCGGGGCCTACGCCCCGCTCACAAAGCATGGGACACTGGTGGTG 723

Qy   1071 GAGGATGTGGTGGCATCCTGCTTCGCGGCCGTGGCTGACCACCACCTGGCTCAGTTGGCC 1130

Db    724 GAGGATGTGGTGGCATCCTGCTTCGCGGCCGTGGCTGACCACCACCTGGCTCAGTTGGCC 783

Qy   1131 TTCTGGCCCCTGAGACTCTTTCACAGCTTGGCATGGGGCAGCTGGACCCCGGGGGAGGGT 1190

Db    784 TTCTGGCCCCTGAGACTCTTTCACAGCTTGGCATGGGGCAGCTGGACCCCGGGGGAGGGT 843

Qy   1191 GTGCATTGGTACCCCCAGCTGCTCTACCGCCTGGGGCGTCTCCTGCTAGAAGAGGGCAGC 1250

Db    844 GTGCATTGGTACCCCCAGCTGCTCTACCGCCTGGGGCGTCTCCTGCTAGAAGAGGGCAGC 903

Qy   1251 TTCCACCCACTGGGCATGTCCGGGGCAGGGAGCTGA 1286

Db    904 TTCCACCCACTGGGCATGTCCGGGGCAGGGAGCTGA 939


RESULT   5
AC016762
LOCUS       AC016762   173557 bp    DNA             HTG       04-DEC-1999
DEFINITION  Homo sapiens clone RP11-540F24, *** SEQUENCING IN PROGRESS ***, 49
            unordered pieces.
ACCESSION   AC016762
VERSION     AC016762.1  GI:6524279
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 173557)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 173557)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-DEC-1999) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     Center project name: H_NH0540F24.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 49 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1     2608: contig of 2608 bp in length
            *    2609     2627: gap of unknown length
            *    2628     4664: contig of 2037 bp in length
            *    4665     4683: gap of unknown length
            *    4684     7270: contig of 2587 bp in length
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*     7271     7289: gap of unknown length
*     7290    10058: contig of 2769 bp in length
*    10059    10077: gap of unknown length
*    10078    12127: contig of 2050 bp in length
*    12128    12146: gap of unknown length
*    12147    14784: contig of 2638 bp in length
*    14785    14803: gap of unknown length
*    14804    16981: contig of 2178 bp in length
*    16982    17000: gap of unknown length
*    17001    18944: contig of 1944 bp in length
*    18945    18963: gap of unknown length
*    18964    21214: contig of 2251 bp in length
*    21215    21233: gap of unknown length
*    21234    25084: contig of 3851 bp in length
*    25085    25103: gap of unknown length
*    25104    28185: contig of 3082 bp in length
*    28186    28204: gap of unknown length
*    28205    31202: contig of 2998 bp in length
*    31203    31221: gap of unknown length
*    31222    34083: contig of 2862 bp in length
*    34084    34102: gap of unknown length
*    34103    37104: contig of 3002 bp in length
*    37105    37123: gap of unknown length
*    37124    40839: contig of 3716 bp in length
*    40840    40858: gap of unknown length
*    40859    43784: contig of 2926 bp in length
*    43785    43803: gap of unknown length
*    43804    48207: contig of 4404 bp in length
*    48208    48226: gap of unknown length
*    48227    51440: contig of 3214 bp in length
*    51441    51459: gap of unknown length
*    51460    53846: contig of 2387 bp in length
*    53847    53865: gap of unknown length
*    53866    56877: contig of 3012 bp in length
*    56878    56896: gap of unknown length
*    56897    59964: contig of 3068 bp in length
*    59965    59983: gap of unknown length
*    59984    63028: contig of 3045 bp in length
*    63029    63047: gap of unknown length
*    63048    66352: contig of 3305 bp in length
*    66353    66371: gap of unknown length
*    66372    70572: contig of 4201 bp in length
*    70573    70591: gap of unknown length
*    70592    74584: contig of 3993 bp in length
*    74585    74603: gap of unknown length
*    74604    79275: contig of 4672 bp in length
*    79276    79294: gap of unknown length
*    79295    83982: contig of 4688 bp in length
*    83983    84001: gap of unknown length
*    84002    88872: contig of 4871 bp in length
*    88873    88891: gap of unknown length
*    88892    94962: contig of 6071 bp in length
*    94963    94981: gap of unknown length
*    94982    99596: contig of 4615 bp in length
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*    99616   104428: contig of 4813 bp in length
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*   104448   111076: contig of 6629 bp in length
*   111077   111095: gap of unknown length
*   111096   116387: contig of 5292 bp in length
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*   116407   121478: contig of 5072 bp in length
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*   121498   127118: contig of 5621 bp in length
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*   134000   134018: gap of unknown length
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*   145556   145573: gap of unknown length
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*   156387   158457: contig of 2071 bp in length
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*   158476   160706: contig of 2231 bp in length
*   160707   160724: gap of unknown length
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*   163023   165634: contig of 2612 bp in length
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*   165653   168077: contig of 2425 bp in length
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*   168096   171233: contig of 3138 bp in length
*   171234   171251: gap of unknown length
*   171252   173557: contig of 2306 bp in length.
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                     /clone="RP11-540F24"
BASE COUNT    47753 a  37720 c  36932 g  50252 t    900 others
ORIGIN


  Query Match            53.6%;  Score 869.4;  DB 43;  Length 173557;
  Best Local Similarity  96.8%;  Pred. No. 7.5e-142;
  Matches  919;  Conservative    0;  Mismatches   26;  Indels    4;  Gaps    3;

Qy     674 CCAGGTACGCCTGGAGAGTGGGGCGCGTGTGGCCTTGTCAGCCGTGAGGCCGGGAGACCG 733
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Db   51637 CCTGGGAAGCTTGTGGAGAGTGGTGCGCGTTGGCCTTGTCAGCGTGAGGCCGGGAGACCG 51696

Qy     734 TGTGCTGGCCATGGGGGAGGATGGGAGCCCCACCTTCAGCGATGTGCTCATTTTCCTGGA 793
           |||||| |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   51697 TGTGCT-GCCATGGGGGAGGAT-GGAGCCCCACCTTCAGCGATGTGCTCATTTTCCTGGA 51754

Qy     794 CCGCGAGCCCCACAGGCTGAGAGCCTTCCAGGTCATCGAGACTCAGGACCCCCCACGCCG 853
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Db   51755 CCGCGAGCCTCACAGGCTGAGAGCCTTCCAGGTCATCGAGACTCAGGACCCCCCACGCCG 51814

Qy     854 CCTGGCACTCACACCCGCTCACCTGCTCTTTACGGCTGACAATCACACGGAGCCGGCAGC 913
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Db   51815 CCTGGCACTCACACCCGCTCACCTGCTCTTTACGGCTGACAATCACACGGAGCCGGCAGC 51874

Qy     914 CCGCTTCCGGGCCACATTTGCCAGCCACGTGCAGCCTGGCCAGTACGTGCTGGTGGCTGG 973
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Db   51875 CCGCTTCCGGGCCACATTTGCCAGCCACGTGCAGCCTGGCCAGTACGTGCTGGTGGCTGG 51934

Qy     974 GGTGCCAGGCCTGCAGCCTGCCCGCGTGGCAGCTGTCTCTACACACGTGGCCCTCGGGGC 1033
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Db   51935 GGTGCCAGGCCTGCAGCCTGCCCGCGTGGCAGCTGTCTCTACACACGTGGCCCTCGGG-- 51993

Qy    1034 CTACGCCCCGCTCACAAAGCATGGGACACTGGTGGTGGAGGATGTGGTGGCATCCTGCTT 1093
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Db   51993 CTACGCCCCGCTCACAAAGCATGGGACACTGGTGGTGGAGGATGTGGTGGCATCCTGCTT 52052

Qy    1094 CGCGGCCGTGGCTGACCACCACCTGGCTCAGTTGGCCTTCTGGCCCCTGAGACTCTTTCA 1153
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Db   52053 CGCGGCCGTGGCTGACCACCACCTGGCTCAGTTGGCCTTCTGGCCCCTGAGACTCTTTCA 52112

Qy    1154 CAGCTTGGCATGGGGCAGCTGGACCCCGGGGGAGGGTGTGCATTGGTACCCCCAGCTGCT 1213
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   52113 CAGCTTGGCATGGGGCAGCTGGACCCCGGGGGAGGGTGTGCATTGGTACCCCCAGCTGCT 52172

Qy    1214 CTACCGCCTGGGGCGTCTCCTGCTAGAAGAGGGCAGCTTCCACCCACTGGGCATGTCCGG 1273
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Db   52173 CTACCGCCTGGGGCGTCTCCTGCTAGAAGAGGGCAGCTTCCACCCACTGGGCATGTCCGG 52232

Qy    1274 GGCAGGGAGCTGAAAGGACTCCACCGCTGCCCTCCTGGAACTGCTGTACTGGGTCCAGAA 1333
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Db  52233 GGCAGGGAGCTGAAAGGACTCCACCGCTGCCCTCCTGGAACTGCTGTACTGGGTCCAGAA 52292

Qy   1334 GCCTCTCAGCCAGGAGGGAGCTGGCCCTGGAAGGGACCTGAGCTGGGGGACACTGGCTCC 1393

Db  52293 GCCTCTCAGCCAGGAGGGAGCTGGCCCTGGAAGGGACCTGAGCTGGGGGACACTGGCTCC 52352

Qy   1394 TGCCATCTCCTCTGCCATGAAGATACACCATTGAGACTTGACTGGGCAACACCAGCGTCC 1453

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Qy   1454 CCCACCCGCGTCGTGGTGTAGTCATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGGTTGT 1513

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Qy   1514 TGACCCCTCTCTCCTAGAGACCTTGAGGCTGGCACGGCGACTCCCAACTCAGCCTGCTCT 1573

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Qy   1574 CACTACGAGTTTTCATACTCTGCCTCCCCCATTGGGAGGGCCCATTCCC 1622

Db  52533 CACTACGAGTTTTCATACTCTGCCTCCCCCATTGGGAGAGGCCCATTCC 52581


RESULT   6
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LOCUS       AR021200     1056 bp    DNA             PAT       05-DEC-1998
DEFINITION  Sequence 5 from patent US 5789543.
ACCESSION   AR021200
VERSION     AR021200.1  GI:3975815
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1056)
  AUTHORS   Ingham,P.W., McMahon,A.P. and Tabin,C.J.
  TITLE     Vertebrate embryonic pattern-inducing proteins and uses related
            thereto
  JOURNAL   Patent: US 5789543-A 5 04-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .1056
                     /organism="unknown"
BASE COUNT      204 a    321 c    312 g    219 t
ORIGIN


  Query Match           52.0%;  Score 843.2;  DB 5;  Length 1056;
  Best Local Similarity   88.2%;  Pred. No. 8.6e-137;
  Matches  928;  Conservative    0;  Mismatches  123;  Indels    1;  Gaps    1;

Qy     276 GAGCGCTTCAAGGAGCTCACCCCCAATTACAATCCAGACATCATCTTCAAGGACGAGGAG 335

Db       1 GAGCGCTTCAAAGAGCTCACCCCCAACTACAATCCCGACATCATCTTCAAGGACGAGGAG 60

Qy     336 AACACAGGCGCCGACCGCCTCATGACCCAGCGCTGCAAGGACCGCCTGAACTCGCTGGCT 395

Db      61 AACACGGGTGCCGACCGCCTCATGACCCAGCGCTGCAAGGACCGTCTGAACTCACTGGCC 120

Qy     396 ATCTCGGTGATGAACCAGTGGCCCGGTGTGAAGCTGCGGGTGACCGAGGGCTGGGACGAG 455

Db     121 ATCTCTGTCATGAACCAGTGGCCTGGTGTGAAACTGCGGGTGACCGAAGGCCGGGATGAA 180

Qy     456 GACGGCCACCACTCAGAGGAGTCCCTGCATTATGAGGGCCGCGCGGTGGACATCACCACA 515

Db     181 GATGGCCATCACTCAGAGGAGTCTTTACACTATGAGGGCCGCGCGGTGGATATCACCACC 240

Qy     516 TCAGACCGCGACCGCAATAAGTATGGACTGCTGGCGCGCTTGGCAGTGGAGGCCGGCTTT 575

Db     241 TCAGACCGTGACCGAAATAAGTATGGACTGCTGGCGCGCTTAGCAGTGGAGGCCGGCTTC 300

Qy     576 GACTGGGTGTATTACGAGTCAAAGGCCCACGTGCATTGCTCCGTCAAGTCCGAGCACTCG 635

Db     301 GACTGGGTGTATTACGAGTCCAAGGCCCACGTGCATTGCTCTGTCAAGTCTGAGCATTCG 360

Qy     636 GCCGCAGCCAAGACGGGCGGCTGCTTCCCTGCCGGAGCCCAGGTACGCCTGGAGAGTGGG 695

Db     361 GCCGCTGCCAAGACAGGTGGCTGCTTTCCTGCCGGAGCCCAGGTGCGCCTAGAGAACGGG 420

Qy     696 GCGCGTGTGGCCTTGTCAGCCGTGAGGCCGGGAGACCGTGTGCTGGCCATGGGGGAGGAT 755

Db     421 GAGCGTGTGGCCCTGTCAGCTGTAAAGCCAGGAGACCGGGTGCTGGCCATGGGGGAGGAT 480

Qy     756 GGGAGCCCCACCTTCAGCGATGTGCTCATTTTCCTGGACCGCGAGCCCCACAGGCTGAGA 815

Db     481 GGGACCCCCACCTTCAGTGATGTGCTTATTTTCCTGGACCGCGAGCCAAACCGGCTGAGA 540

Qy     816 GCCTTCCAGGTCATCGAGACTCAGGACCCCCCACGCCGCCTGGCACTCACACCCGCTCAC 875

Db     541 GCTTTCCAGGTCATCGAGACTCAGGATCCTCCGCGTCGGCTGGCGCTCACGCCTGCCCAC 600

Qy     876 CTGCTCTTTACGGCTGACAATCACACGGAGCCGGCAGCCCGCTTCCGGGCCACATTTGCC 935

Db     601 CTGCTCTTCATTGCGGACAATCATACAGAACCAGCAGCCCACTTCCGGGCCACATTTGCC 660

Qy     936 AGCCACGTGCAGCCTGGCCAGTACGTGCTGGTGGCTGGGGTGCCAGGCCTGCAGCCTGCC 995

Db     661 AGCCATGTGCAACCAGGCCAATATGTGCTGGTATCAGGGGTACCAGGCCTCCAGCCTGCT 720

Qy     996 CGCGTGGCAGCTGTCTCTACACACGTGGCCCTCGGGGCCTACGCCCCGCTCACAAAGCAT 1055

Db     721 CGGGTGGCAGCTGTCTCCACCCACGTGGCCCTTGGGTCCTATGCTCCTCTCACAAGGCAT 780

Qy    1056 GGGACACTGGTGGTGGAGGATGTGGTGGCATCCTGCTTCGCGGCCGTGGCTGACCACCAC 1115

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Qy    1176 ACCCCGGGGGAGGGTGTGCATTGGTACCCCCAGCTGCTCTACCGCCTGGGGCGTCTCCTG 1235

Db     901 ACCCCAAGTGAGGGTGTTCACTCCTACCCTCAGATGCTCTACCGCCTGGGGCGTCTCTTG 960

Qy    1236 CTAGAAGAGGGCAGCTTCCACCCACTGGGCATGTCCGGGGCAGGGAGCTGAAAGGACTC- 1295

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Qy    1295 CACCGCTGCCCTCCTGGAACTGCTGTACTGGG 1326

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RESULT   7
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LOCUS       AR063082     1056 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 3 from patent US 5844079.
ACCESSION   AR063082
VERSION     AR063082.1  GI:5990773
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1056)
  AUTHORS   Ingham,P.W., McMahon,A.P. and Tabin,C.J.
  TITLE     Vertebrate embryonic pattern-inducing proteins, and uses related
            thereto
  JOURNAL   Patent: US 5844079-A 3 01-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .1056
                     /organism="unknown"
BASE COUNT      204 a    321 c    312 g    219 t
ORIGIN


  Query Match           52.0%;  Score 843.2;  DB 5;  Length 1056;
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 Best Local Similarity   88.2%;  Pred. No. 8.6e-137;
 Matches  928;  Conservative    0;  Mismatches  123;  Indels    1;  Gaps    1;

Qy    276 GAGCGCTTCAAGGAGCTCACCCCCAATTACAATCCAGACATCATCTTCAAGGACGAGGAG 335
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Qy    336 AACACAGGCGCCGACCGCCTCATGACCCAGCGCTGCAAGGACCGCCTGAACTCGCTGGCT 395
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Db     61 AACACGGGTGCCGACCGCCTCATGACCCAGCGCTGCAAGGACCGTCTGAACTCACTGGCC 120

Qy    396 ATCTCGGTGATGAACCAGTGGCCCGGTGTGAAGCTGCGGGTGACCGAGGGCTGGGACGAG 455
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Db    121 ATCTCTGTCATGAACCAGTGGCCTGGTGTGAAACTGCGGGTGACCGAAGGCCGGGATGAA 180

Qy    456 GACGGCCACCACTCAGAGGAGTCCCTGCATTATGAGGGCCGCGCGGTGGACATCACCACA 515
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Db    181 GATGGCCATCACTCAGAGGAGTCTTTACACTATGAGGGCCGCGCGGTGGATATCACCACC 240

Qy    516 TCAGACCGCGACCGCAATAAGTATGGACTGCTGGCGCGCTTGGCAGTGGAGGCCGGCTTT 575
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Db    241 TCAGACCGTGACCGAAATAAGTATGGACTGCTGGCGCGCTTAGCAGTGGAGGCCGGCTTC 300

Qy    576 GACTGGGTGTATTACGAGTCAAAGGCCCACGTGCATTGCTCCGTCAAGTCCGAGCACTCG 635
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Db    301 GACTGGGTGTATTACGAGTCCAAGGCCCACGTGCATTGCTCTGTCAAGTCTGAGCATTCG 360

Qy    636 GCCGCAGCCAAGACGGGCGGCTGCTTCCCTGCCGGAGCCCAGGTACGCCTGGAGAGTGGG 695
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Db    361 GCCGCTGCCAAGACAGGTGGCTGCTTTCCTGCCGGAGCCCAGGTGCGCCTAGAGAACGGG 420

Qy    696 GCGCGTGTGGCCTTGTCAGCCGTGAGGCCGGGAGACCGTGTGCTGGCCATGGGGGAGGAT 755
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Db    421 GAGCGTGTGGCCCTGTCAGCTGTAAAGCCAGGAGACCGGGTGCTGGCCATGGGGGAGGAT 480

Qy    756 GGGAGCCCCACCTTCAGCGATGTGCTCATTTTCCTGGACCGCGAGCCCCACAGGCTGAGA 815
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Db    481 GGGACCCCCACCTTCAGTGATGTGCTTATTTTCCTGGACCGCGAGCCAAACCGGCTGAGA 540

Qy    816 GCCTTCCAGGTCATCGAGACTCAGGACCCCCCACGCCGCCTGGCACTCACACCCGCTCAC 875
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Db    541 GCTTTCCAGGTCATCGAGACTCAGGATCCTCCGCGTCGGCTGGCGCTCACGCCTGCCCAC 600

Qy    876 CTGCTCTTTACGGCTGACAATCACACGGAGCCGGCAGCCCGCTTCCGGGCCACATTTGCC 935
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Db    601 CTGCTCTTCATTGCGGACAATCATACAGAACCAGCAGCCCACTTCCGGGCCACATTTGCC 660

Qy    936 AGCCACGTGCAGCCTGGCCAGTACGTGCTGGTGGCTGGGGTGCCAGGCCTGCAGCCTGCC 995
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Db    661 AGCCATGTGCAACCAGGCCAATATGTGCTGGTATCAGGGGTACCAGGCCTCCAGCCTGCT 720

Qy    996 CGCGTGGCAGCTGTCTCTACACACGTGGCCCTCGGGGCCTACGCCCCGCTCACAAAGCAT 1055
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Qy   1056 GGGACACTGGTGGTGGAGGATGTGGTGGCATCCTGCTTCGCGGCCGTGGCTGACCACCAC 1115
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Db    781 GGGACACTTGTGGTGGAGGATGTGGTGGCCTCCTGCTTTGCAGCTGTGGCTGACCACCAT 840

Qy   1116 CTGGCTCAGTTGGCCTTCTGGCCCCTGAGACTCTTTCACAGCTTGGCATGGGGCAGCTGG 1175
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Db    841 CTGGCTCAGTTGGCCTTCTGGCCCCTGCGACTGTTTCCCAGTTTGGCATGGGGCAGCTGG 900

Qy   1176 ACCCCGGGGGAGGGTGTGCATTGGTACCCCCAGCTGCTCTACCGCCTGGGGCGTCTCCTG 1235
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Qy   1236 CTAGAAGAGGGCAGCTTCCACCCACTGGGCATGTCCGGGGCAGGGAGCTGAAAGGACTC- 1295
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Db    961 CTAGAAGAGAGCACCTTCCATCCACTGGGCATGTCTGGGGCAGGAAGCTGAAGGGACTCT 1020

Qy   1295 CACCGCTGCCCTCCTGGAACTGCTGTACTGGG 1326
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Db   1021 AACCACTGCCCTCCTGGAACTGCTGTGCGTGG 1052


RESULT   8
MMIHH
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DEFINITION  M.musculus (C57BL/6J) Ihh mRNA.
ACCESSION   X76291
VERSION     X76291.1  GI:2440120
KEYWORDS    ihh gene; indian hedgehog protein.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1011)
  AUTHORS   McMahon,A.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-NOV-1993) A.P. McMahon, Harvard University, 16
            Divinity Ave., Cambridge, MA 02138, USA
  REMARK    revised by [3]
REFERENCE   2  (bases 1 to 1011)
  AUTHORS   Echelard,Y., Epstein,D.J., St-Jacques,B., Shen,L., Mohler,J.,
            McMahon,J.A. and McMahon,A.P.
  TITLE     Sonic hedgehog, a member of a family of putative signaling
            molecules, is implicated in the regulation of CNS polarity
  JOURNAL   Cell 75 (7), 1417-1430 (1993)
  MEDLINE   94094334
REFERENCE   3  (bases 1 to 1011)
  AUTHORS   St-Jacques,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-APR-1997) B. St-Jacques, Harvard University, 16
            Divinity Ave., Cambridge, MA 02138, USA
  REMARK    revised by author 25-SEP-97
COMMENT     On Sep 27, 1997 this sequence version replaced gi:1938224.
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                     /db_xref="taxon:10090"
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                     /clone_lib="Hogan; lambda gt10"
     gene            1. .1011
                     /gene="Ihh"
     CDS             <1. .1011
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                     /product="indian hedgehog"
                     /protein_id="CAA53923.1"
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                     GTPTFSDVLIFLDREPNRLRAFQVIETQDPPRRLALTPAHLLFIADNHTEPAAHFRAT
                     FASHVQPGQYVLVSGVPGLQPARVAAVSTHVALGSYAPLTRHGTLVVEDVVASCFAAV
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                     GS"
BASE COUNT      196 a    303 c    302 g    210 t
ORIGIN


  Query Match           51.1%;  Score 828.6;  DB 12;  Length 1011;
  Best Local Similarity   88.7%;  Pred. No. 2.9e-134;
  Matches  897;  Conservative    0;  Mismatches  114;  Indels    0;  Gaps    0;

Qy    276 GAGCGCTTCAAGGAGCTCACCCCCAATTACAATCCAGACATCATCTTCAAGGACGAGGAG 335
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Db      1 GAGCGCTTCAAAGAGCTCACCCCCAACTACAATCCCGACATCATCTTCAAGGACGAGGAG 60

Qy    336 AACACAGGCGCCGACCGCCTCATGACCCAGCGCTGCAAGGACCGCCTGAACTCGCTGGCT 395
          ||||| || |||||||||||||||||||||||||||||||||||||| |||||||| |||||
Db     61 AACACGGGTGCCGACCGCCTCATGACCCAGCGCTGCAAGGACCGTCTGAACTCACTGGCC 120
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Qy    396 ATCTCGGTGATGAACCAGTGGCCCGGTGTGAAGCTGCGGGTGACCGAGGGCTGGGACGAG 455
Db    121 ATCTCTGTCATGAACCAGTGGCCTGGTGTGAAACTGCGGGTGACCGAAGGCTGGGATGAA 180

Qy    456 GACGGCCACCACTCAGAGGAGTCCCTGCATTATGAGGGCCGCGCGGTGGACATCACCACA 515
Db    181 GATGGCCATCACTCAGAGGAGTCTTTACACTATGAGGGCCGCGCGGTGGATATCACCACC 240

Qy    516 TCAGACCGCGACCGCAATAAGTATGGACTGCTGGCGCGCTTGGCAGTGGAGGCCGGCTTT 575
Db    241 TCAGACCGTGACCGAAATAAGTATGGACTGCTGGCGCGCTTAGCAGTGGAGGCCGGCTTC 300

Qy    576 GACTGGGTGTATTACGAGTCAAAGGCCCACGTGCATTGCTCCGTCAAGTCCGAGCACTCG 635
Db    301 GACTGGGTGTATTACGAGTCCAAGGCCCACGTGCATTGCTCTGTCAAGTCTGAGCATTCG 360

Qy    636 GCCGCAGCCAAGACGGGCGGCTGCTTCCCTGCCGGAGCCCAGGTACGCCTGGAGAGTGGG 695
Db    361 GCCGCTGCCAAGACAGGTGGCTGCTTTCCTGCCGGAGCCCAGGTGCGCCTAGAGAACGGG 420

Qy    696 GCGCGTGTGGCCTTGTCAGCCGTGAGGCCGGGAGACCGTGTGCTGGCCATGGGGGAGGAT 755
Db    421 GAGCGTGTGGCCCTGTCAGCTGTAAAGCCAGGAGACCGGGTGCTGGCCATGGGGGAGGAT 480

Qy    756 GGGAGCCCCACCTTCAGCGATGTGCTCATTTTCCTGGACCGCGAGCCCCACAGGCTGAGA 815
Db    481 GGGACCCCCACCTTCAGTGATGTGCTTATTTTCCTGGACCGCGAGCCAAACCGGCTGAGA 540

Qy    816 GCCTTCCAGGTCATCGAGACTCAGGACCCCCCACGCCGCCTGGCACTCACACCCGCTCAC 875
Db    541 GCTTTCCAGGTCATCGAGACTCAGGATCCTCCGCGTCGGCTGGCGCTCACGCCTGCCCAC 600

Qy    876 CTGCTCTTTACGGCTGACAATCACACGGAGCCGGCAGCCCGCTTCCGGGCCACATTTGCC 935
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Qy    936 AGCCACGTGCAGCCTGGCCAGTACGTGCTGGTGGCTGGGGTGCCAGGCCTGCAGCCTGCC 995
Db    661 AGCCATGTGCAACCAGGCCAATATGTGCTGGTATCAGGGGTACCAGGCCTCCAGCCTGCT 720

Qy    996 CGCGTGGCAGCTGTCTCTACACACGTGGCCCTCGGGGCCTACGCCCCGCTCACAAAGCAT 1055
Db    721 CGGGTGGCAGCTGTCTCCACCCACGTGGCCCTTGGGTCCTATGCTCCTCTCACAAGGCAT 780

Qy   1056 GGGACACTGGTGGTGGAGGATGTGGTGGCATCCTGCTTCGCGGCCGTGGCTGACCACCAC 1115
Db    781 GGGACACTTGTGGTGGAGGATGTGGTGGCCTCCTGCTTTGCAGCTGTGGCTGACCACCAT 840

Qy   1116 CTGGCTCAGTTGGCCTTCTGGCCCCTGAGACTCTTTCACAGCTTGGCATGGGGCAGCTGG 1175
Db    841 CTGGCTCAGTTGGCCTTCTGGCCCCTGCGACTGTTTCCCAGTTTGGCATGGGGCAGCTGG 900

Qy   1176 ACCCCGGGGGAGGGTGTGCATTGGTACCCCCAGCTGCTCTACCGCCTGGGGCGTCTCCTG 1235
Db    901 ACCCCAAGTGAGGGTGTTCACTGGTACCCTCAGATGCTCTACCGCCTGGGGCGTCTCTTG 960

Qy   1236 CTAGAAGAGGGCAGCTTCCACCCACTGGGCATGTCCGGGGCAGGGAGCTGA 1286
Db    961 CTAGAAGAGAGCACCTTCCATCCACTGGGCATGTCTGGGGCAGGAAGCTGA 1011
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RESULT   9
GGU58511
LOCUS       GGU58511     1958 bp    mRNA            VRT       16-AUG-1996
DEFINITION  Gallus gallus indian hedgehog protein mRNA, complete cds.
ACCESSION   U58511
VERSION     U58511.1  GI:1493841
KEYWORDS    .
SOURCE      chicken.
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
            Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 1958)
  AUTHORS   Vortkamp,A., Lee,K., Lanske,B., Segre,G.V., Kronenberg,H.M. and
            Tabin,C.J.
  TITLE     Regulation of rate of cartilage differentiation by Indian hedgehog
            and PTH-related protein
  JOURNAL   Science 273 (5275), 613-622 (1996)
  MEDLINE   96325423
REFERENCE   2  (bases 1 to 1958)
  AUTHORS   Vortkamp,A., Lee,K., Lanske,B., Segre,G.V., Kronenberg,H.M. and
            Tabin,C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-MAY-1996) A. Vortkamp, Genetics, Harvard Medical
            School, 200 Longwood, Boston, MA 02115, USA
FEATURES             Location/Qualifiers
     source          1. .1958
                     /organism="Gallus gallus"
                     /db_xref="taxon:9031"
     CDS             328. .1554
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                     /product="indian hedgehog protein"
                     /protein_id="AAC60010.1"
                     /db_xref="GI:1493842"
                     /translation="MKPARLLLLLSGCALLLAPAVRCCGPGRVVGSRRRPPRKLIPLA
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                     MLARLAVEAGFDWVYYESKAHIHCSVKSEHSAAAKTGGCFPGRALATLENGARTPLWA
                     LRPGQRVLAMDGAGRPTYSDFLAFLDKEPRALTAFHVIETRQPPRRLALTPTHLLFVA
                     DNASAPAAQFRPTFASHVQPGHFVLVAVGSGGLQPAEVVGVRGRTDVGAYAPLTRHGT
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                     LPPDSFHPLGAPRAES"
BASE COUNT      279 a    677 c    740 g    260 t      2 others
ORIGIN
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Query Match 46.7%; Score 757.4; DB 4; Length 1958;
Best Local Similarity 75.5%; Pred. No. 5.1e-122;
Matches 954; Conservative 0; Mismatches 306; Indels 3; Gaps 1;

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Qy     40 GCTCCCCGGCCATGTCTCCCGCCCGGCTCCGGCCCCGACTGCACTTCTGCCTGGTCCTGT 99
Db    305 GCCCCGGGGCCGCCGGGCGCGCCATGAAGCCGGCGCGGCTGCTGCTGCTGCTGAGCGGGT 364

Qy    100 TGCTGCTGCTGGTGGTGCCCGCGGCATGGGGCTGCGGGCCGGGTCGGGTGGTGGGCAGCC 159
Db    365 GCGCGCTGCTGCTGGCGCCGGCCGTGCGCTGCTGCGGGCCGGGCAGGGTTGTGGGCAGCC 424

Qy    160 GCCGGCGACCGCCACGCAAACTCGTGCCGCTCGCCTACAAGCAGTTCAGCCCCAATGTGC 219
Db    425 GCCGCCGGCCGCCCCGCAAGCTCATCCCGCTCGCCTACAAGCAGTTCAGCCCCAACGTGC 484

Qy    220 CCGAGAAGACCCTGGGCGCCAGCGGACGCTATGAAGGCAAGATCGCTCGCAGCTCCGAGC 279
Db    485 CCGAGAAGACGCTGGGGGCCAGCGGGCGCTACGAGGGCAAGATCGCGCGGAACTCGGAGC 544

Qy    280 GCTTCAAGGAGCTCACCCCCAATTACAATCCAGACATCATCTTCAAGGACGAGGAGAACA 339
Db    545 GCTTCAAGGAGCTCACGCCCAACTACAACCCCGACATCATCTTCAAGGACGAGGAGAACA 604

Qy    340 CAGGCGCCGACCGCCTCATGACCCAGCGCTGCAAGGACCGCCTGAACTCGCTGGCTATCT 399
Db    605 CCGGCGCCGACCGGCTCATGACCCAGCGCTGCAAGGACCGCCTGAACTCCCTGGCCATCT 664

Qy    400 CGGTGATGAACCAGTGGCCCGGTGTGAAGCTGCGGGTGACCGAGGGCTGGGACGAGGACG 459
Db    665 CCGTCATGAACCAGTGGCCGGGGGTGAAGCTGCGGGTGACGGAGGGCTGGGATGAGGACG 724

Qy    460 GCCACCACTCAGAGGAGTCCCTGCATTATGAGGGCCGCGCGGTGGACATCACCACATCAG 519
Db    725 GCCACCACTCGGAGGAGTCGCTGCATTACGAGGGCCGAGCCGTGGACATCACGACGTCAG 784

Qy    520 ACCGCGACCGCAATAAGTATGGACTGCTGGCGCGCTTGGCAGTGGAGGCCGGCTTTGACT 579
Db    785 ACAGGGACCGCAACAAGTACGGCATGCTTGCCCGCCTGGCTGTGGAGGCCGGCTTTGACT 844
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Qy     580 GGGTGTATTACGAGTCAAAGGCCCACGTGCATTGCTCCGTCAAGTCCGAGCACTCGGCCG 639
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Db     845 GGGTCTACTACGAGTCCAAGGCGCACATCCACTGCTCCGTCAAGTCAGAGCACTCGGCTG 904

Qy     640 CAGCCAAGACGGGCGGCTGCTTCCCTGCCGGAGCCCAGGTACGCCTGGAGAGTGGGGCGC 699
           | || ||||||||||||||||||| |   | || | ||     |||||| || || |
Db     905 CCGCGAAGACGGGCGGCTGCTTCCCCGGGCGGGCGCTGGCGACGCTGGAGAACGGTGCCC 964

Qy     700 GTGTGGCCTTGTCAGCCGTGAGGCCGGGAGACCGTGTGCTGGCCATGGGGGAGGATGGGA 759
           |   | |  |||  ||  || |||||||  | || |||||||| ||||  | ||  ||
Db     965 GGACGCCACTGTGGGCACTGCGGCCGGGCCAGCGGGTGCTGGCGATGGACGGGGCGGGCC 1024

Qy     760 GCCCCACCTTCAGCGATGTGCTCATTTTCCTGGACCGCGAGCCCCACAGGCTGAGAGCCT 819
           | ||||||| ||||||  | ||    |||||||||   ||||| | |   || |  ||||
Db    1025 GGCCCACCTACAGCGACTTCCTGGCCTTCCTGGACAAGGAGCCGCGCGCCCTCACTGCCT 1084

Qy     820 TCCAGGTCATCGAGACTCAGGACCCCCCACGCCGCCTGGCACTCACACCCGCTCACCTGC 879
           |||| |||||||||||| | | | || || || |||||||| || || ||| | |||||||
Db    1085 TCCACGTCATCGAGACGCGGCAGCCGCCCCGGCGCCTGGCCCTGACGCCCACCCACCTGC 1144

Qy     880 TCTTTACGGCTGACAATCACACGGAGCCGGCAGCCCGCTTCCGGGCCACATTTGCCAGCC 939
           ||||   ||| ||||||   | ||| ||| || ||||  |||||  |||| || |||||||
Db    1145 TCTTCGTGGCCGACAACGCCTCGGCGCCCGCCGCCCAATTCCGCCCCACCTTCGCCAGCC 1204

Qy     940 ACGTGCAGCCTGGCCAGTACGTGCTGGTGGCTGGGG---TGCCAGGCCTGCAGCCTGCCC 996
           |||||||||| || || | |||||||||||| | ||    |   || |||||||| |||
Db    1205 ACGTGCAGCCCGGACACTTCGTGCTGGTGGCGGTGGGCTCGGGGGGGCTGCAGCCCGCCG 1264

Qy     997 GCGTGGCAGCTGTCTCTACACACGTGGCCCTCGGGGCCTACGCCCCGCTCACAAAGCATG 1056
             ||||  |  ||       |    || | | ||||| |||||||||| ||    || |
Db    1265 AAGTGGTGGGGGTGAGGGGCCGGACGGACGTGGGGGCTTACGCCCCGCTGACGCGACACG 1324

Qy    1057 GGACACTGGTGGTGGAGGATGTGGTGGCATCCTGCTTCGCGGCCGTGGCTGACCACCACC 1116
           |||| |||||||||| || |||||||| || |||||||     |||   || || || |
Db    1325 GGACGCTGGTGGTGGACGACGTGGTGGCCTCGTGCTTCGCCCTGGTGCGGGAGCAGCAGC 1384

Qy    1117 TGGCTCAGTTGGCCTTCTGGCCCCTGAGACTCTTTCACAGCTTGGCATGGGGCAGCTGGA 1176
           |||| ||| |||||||||||| ||| | || |  |||||| ||    ||||     ||
Db    1385 TGGCGCAGATGGCCTTCTGGCCGCTGCGGCTGTACCACAGCCTGCTGGGGGGGCCGGGGG 1444

Qy    1177 CCCCGGGGGAGGGTGTGCATTGGTACCCCCAGCTGCTCTACCGCCTGGGGCGTCTCCTGC 1236
             | ||| || |||||||| ||||||  |   |||||||||||||||||  | | ||||
Db    1445 TGCAGGGCGACGGTGTGCACTGGTACTCGGGGCTGCTCTACCGCCTGGGCAGGATGCTGC 1504

Qy    1237 TAGAAGAGGGCAGCTTCCACCCACTGGGCATGTCCGGGGCAGGGAGCTGAAAGGACTCCA 1296
           |       | ||||||||||| |||||    | || |||| | |||||||  |    ||
Db    1505 TGCCCCCCGACAGCTTCCACCCGCTGGGGGCGCCCCGGGCCGAGAGCTGAGGGTGTACCG 1564

Qy    1297 CCG 1299
           |||
Db    1565 GCG 1567


RESULT 10
AB010092S3
LOCUS       AB010092S3    683 bp    DNA             PRI       07-JAN-2000
DEFINITION  Homo sapiens hedgehog gene, exon 3 and complete cds.
ACCESSION   AB018076
VERSION     AB018076.1  GI:3702726
KEYWORDS    hedgehog.
SEGMENT     3 of 3
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Tate,G., Kishimoto,K. and Mitsuya,T.
  TITLE     Expression of Sonic hedgehog and its receptor Patched/Smoothened in
            human cancer cell lines and embryonic organs
  JOURNAL   J. Biochem. Mol. Biol. Biophys. 4, 27-34 (2000)
REFERENCE   2  (bases 1 to 683)
  AUTHORS   Tate,G., Endo,Y. and Mitsuya,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-SEP-1998) to the DDBJ/EMBL/GenBank databases. Genshu
            Tate, Showa University Fujigaoka Hospital, Department of Surgical
            Pathology; Fujigaoka 1-30, Aoba-ku, Yokohama, Kanagawa 227-8501,
            Japan (E-mail:six10352@super.win.or.jp, Tel:81-45-974-6632,
            Fax:81-45-972-6242)
FEATURES             Location/Qualifiers
     source          1. .683
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     gene            join(AB010092.1:1. .315,AB018075.1:1. .283,1. .671)
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                     NKYGLLARLAVEAGFDWVYYESKAHVHCSVKSEHSAAAKTGGCFPAGAQVRLESGARV
                     ALSAVRPGDRVLAMGEDGSPTFSDVIILLDREPHRLRAFQFIETQDPPRRLALTPAHL
                     LFTADNHTEPAARFRATFASHVQPGQYVLVAGVPGLQPARVAAVSTHVALGAYAPLTK
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     exon            13. .671
                     /gene="hedgehog"
                     /number=3
BASE COUNT      107 a    227 c    222 g    127 t
ORIGIN


  Query Match             40.8%;  Score 661.2;  DB 9;  Length 683;
  Best Local Similarity   98.8%;  Pred. No. 2.8e-105;
  Matches  666;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy     625 CCGAGCACTCGGCCGCAGCCAAGACGGGCGGCTGCTTCCCTGCCGGAGCCCAGGTACGCC 684
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10 CAGAGCACTCGGCCGCAGCCAAGACGGGCGGCTGCTTCCCTGCCGGAGCCCAGGTACGCC 69

Qy     685 TGGAGAGTGGGGCGCGTGTGGCCTTGTCAGCCGTGAGGCCGGGAGACCGTGTGCTGGCCA 744
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db      70 TGGAGAGTGGGGCGCGTGTGGCCTTGTCAGCCGTGAGGCCGGGAGACCGTGTGTTGGCCA 129

Qy     745 TGGGGGAGGATGGGAGCCCCACCTTCAGCGATGTGCTCATTTTCCTGGACCGCGAGCCCC 804
           |||||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||
Db     130 TGGGGGAGGATGGGAGCCCCACCTTCAGCGATGTGATCATTTTACTGGACCGCGAGCCCC 189

Qy     805 ACAGGCTGAGAGCCTTCCAGGTCATCGAGACTCAGGACCCCCCACGCCGCCTGGCACTCA 864
           |||||||||||||||| ||| ||||||||||||||||||||||||||| |||||||||
Db     190 ACAGGCTGAGAGCCTTTCAGTTCATCGAGACTCAGGACCCCCCACGCCGCTTGGCACTCA 249

Qy     865 CACCCGCTCACCTGCTCTTTACGGCTGACAATCACACGGAGCCGGCAGCCCGCTTCCGGG 924
           |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     250 CACCCGCTCACTTGCTCTTTACGGCTGACAATCACACGGAGCCGGCAGCCCGCTTCCGGG 309

Qy     925 CCACATTTGCCAGCCACGTGCAGCCTGGCCAGTACGTGCTGGTGGCTGGGGTGCCAGGCC 984
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     310 CCACATTTGCCAGCCACGTGCAGCCTGGCCAGTACGTGCTGGTGGCTGGGGTGCCAGGCC 369

Qy     985 TGCAGCCTGCCCGCGTGGCAGCTGTCTCTACACACGTGGCCCTCGGGGCCTACGCCCCGC 1044
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     370 TGCAGCCTGCCCGCGTGGCAGCTGTCTCTACACACGTGGCCCTCGGGGCCTACGCCCCGC 429

Qy    1045 TCACAAAGCATGGGACACTGGTGGTGGAGGATGTGGTGGCATCCTGCTTCGCGGCCGTGG 1104
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     430 TCACAAAGCATGGGACACTGGTGGTGGAGGATGTGGTGGCATCCTGCTTCGCGGCCGTGG 489

Qy    1105 CTGACCACCACCTGGCTCAGTTGGCCTTCTGGCCCCTGAGACTCTTTCACAGCTTGGCAT 1164
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     490 CTGACCACCACCTGGCTCAGTTGGCCTTCTGGCCCCTGAGACTCTTTCACAGCTTGGCAT 549

Qy    1165 GGGGCAGCTGGACCCCGGGGGAGGGTGTGCATTGGTACCCCCAGCTGCTCTACCGCCTGG 1224
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Db    550 GGGGCAGCTGGACCCCGGGGGAGGGTGTGCATTGGTACCCCCAGCTGCTCTACCGCCTGG 609

Qy   1225 GGCGTCTCCTGCTAGAAGAGGGCAGCTTCCACCCACTGGGCATGTCCGGGGCAGGGAGCT 1284

Db    610 GGCGTCTCCTGCTAGAAGAGGGCAGCTTCCACCCACTGGGCATGTCCGGGGCAGGGAGCT 669

Qy   1285 GAAAGGACTCCACC 1298

Db    670 GAAAGGACTCCACC 683


RESULT 11
AF047466
LOCUS       AF047466     1635 bp    mRNA            VRT       19-FEB-1998
DEFINITION  Notophthalmus viridescens hedgehog segment polarity homolog mRNA,
            complete cds.
ACCESSION   AF047466
VERSION     AF047466.1  GI:2896034
KEYWORDS    .
SOURCE      eastern newt.
  ORGANISM  Notophthalmus viridescens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
            Batrachia; Caudata; Salamandroidea; Salamandridae; Notophthalmus.
REFERENCE   1  (bases 1 to 1635)
  AUTHORS   Stark,D.R., Gates,P.B., Brockes,J.P. and Ferretti,P.
  TITLE     Hedgehog homologue from Notophthalmus viridescens
  JOURNAL   Dev. Dyn. (1998) In press
REFERENCE   2  (bases 1 to 1635)
  AUTHORS   Stark,D.R., Gates,P.B., Brockes,J.P. and Ferretti,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-FEB-1998) MBB, The Krebs Institute, Western Bank,
            Sheffield S10 2TN, UK
FEATURES             Location/Qualifiers
     source          1. .1635
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                     /db_xref="taxon:8316"
     CDS             1. .1221
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                     Number L02793"
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                     /product="hedgehog segment polarity homolog"
                     /protein_id="AAC03108.1"
                     /db_xref="GI:2896035"
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                     MLARLAAEAGFDWVYYESKAHIHCSVKSEHSAAAKTGGCFPARALATLESGEKIPIAD
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                     DNFTVPLTDFSTVFASHVQPGQYILTEGVLGLQPARVVSVTTQTDSGAYAPLTSHGTL
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BASE COUNT      368 a    455 c    482 g    330 t
ORIGIN


  Query Match             38.2%;  Score 618.8;  DB 4;  Length 1635;
  Best Local Similarity   70.3%;  Pred. No. 4.9e-98;
  Matches  859;  Conservative    0;  Mismatches  357;  Indels    6;  Gaps    2;

Qy      65 GCTCCGGCCCCGACTGCACTTCTGCCTGGTCCTGTTGCTGCTGCTGGTGGTGCCCGCGGC 124

Db       6 GCTGCTGGCCCTCCCACTGCTGGCCGTGGCGTGCGCTCTGCTGCTGGGGGGCCCCGGGGC 65

Qy     125 ATGGGGCTGCGGGCCGGGTCGGGTGGTGGGCAGCCGCCGGCGACCGCCACGCAAACTCGT 184

Db      66 GCTGGGCTGCGGGCCTGGCAGGGTGATCGGCCGCCGACCGAGGCCCCCGAGG---CTTAT 122

Qy     185 GCCGCTCGCCTACAAGCAGTTCAGCCCCAATGTGCCCGAGAAGACCCTGGGCGCCAGCGG 244

Db     123 CCCGCTCTCCTACAAGCAGTTCCTGCCCCACGTGCCCGAGAAGACCCTGGGGGCCAGTGG 182

Qy     245 ACGCTATGAAGGCAAGATCGCTCGCAGCTCCGAGCGCTTCAAGGAGCTCACCCCCAATTA 304

Db     183 GCGCTATGAGGGCAAGATCGCCCGCAACTCGGAGCGCTTCAAGGAGTTGACGCCCAACTA 242

Qy     305 CAATCCAGACATCATCTTCAAGGACGAGGAGAACACAGGCGCCGACCGCCTCATGACCCA 364

Db     243 CAACCCGGACATCATCTTCAAGGACGAGGAGAACACGGGGGCGGACCGGATCATGACCCA 302

Qy     365 GCGCTGCAAGGACCGCCTGAACTCGCTGGCTATCTCGGTGATGAACCAGTGGCCCGGTGT 424

Db     303 GCGCTGCAAAGACCGGCTTAACTCCCTGGCCATTTCAGTCATGAACCAGTGGCCCGGGGT 362

Qy     425 GAAGCTGCGGGTGACCGAGGGCTGGGACGAGGACGGCCACCACTCAGAGGAGTCCCTGCA 484

Db     363 CAAACTGCGGGTCACCGAGGGCTGGGATGAAGATGGTCACCACTCTGACGAGTCGCTGCA 422

Qy     485 TTATGAGGGCCGCGCGGTGGACATCACCACATCAGACCGCGACCGCAATAAGTATGGACT 544

Db     423 CTACGAAGGACGAGCGGTGGATATTACCACCTCAGACCGGGACCGTAACAAGTACGGCAT 482

Qy     545 GCTGGCGCGCTTGGCAGTGGAGGCCGGCTTTGACTGGGTGTATTACGAGTCAAAGGCCCA 604

Db     483 GCTGGCCCGGCTAGCGGCGGAAGCCGGATTCGACTGGGTCTACTACGAGTCCAAGGCGCA 542

Qy     605 CGTGCATTGCTCCGTCAAGTCCGAGCACTCGGCCGCAGCCAAGACGGGCGGCTGCTTCCC 664

Db     543 CATCCACTGTTCGGTGAAGTCCGAACACTCTGCTGCAGCAAAGACAGGCGGCTGCTTCCC 602

Qy     665 TGCCGGAGCCCAGGTACGCCTGGAGAGTGGGGCGCGTGTGGCCTTGTCAGCCGTGAGGCC 724

Db     603 TGCAAGGGCCCTGGCAACGCTGGAGAGTGGCGAGAAGATCCCCATCGCAGATCTGGAACC 662

Qy     725 GGGAGACCGTGTGCTGGCCATGGGGGAGGATGGGAGCCCCACCTTCAGCGATGTGCTCAT 784

Db     663 TGGTCATCGAGTGTTGTGCATGGATGAGGGCGGCCGCAGAACCTACAGCGATTTCTTAAC 722

Qy     785 TTTCCTGGACCGCGAGCCCCACAGGCTGAGAGCCTTCCAGGTCATCGAGACTCAGGACCC 844

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Qy     965 GGTGGCTGGGGTGCCAGGCCTGCAGCCTGCCCGCGTGGCAGCTGTCTCTACACACGTGGC 1024

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Db     963 CTCAGGTGCTTACGCACCCCTCACGAGCCATGGCACGTTGCTGGTAGACGATGTAGTCGT 1022

Qy    1085 ATCCTGCTTCGCGGCCGTGGCTGACCACCACCTGGCTCAGTTGGCCTTCTGGCCCCTGAG 1144

Db    1023 ATCCTGCTTTGCTGTGGTCCAAAAGCATCAGCTGGCACAGCTCGCCTTCTGGCCACTGCG 1082

Qy    1145 ACTCTTTCACAGCTTGGCATGGGGCAGCTGGACCCCGGGGGAGGGTGTGCATTGGTACCC 1204

Db    1083 ACTTTACCACAGCGTGG---GTAGGCCAGAGACACAGCCAGAGGGCATGCACTGGTACTC 1139

Qy    1205 CCAGCTGCTCTACCGCCTGGGGCGTCTCCTGCTAGAAGAGGGCAGCTTCCACCCACTGGG 1264

Db    1140 ACTACTTCTTTACCGGCTTGGCAAGGTGTTGCTCATGAAGGAACAGTTCCACCCTTTTGG 1199

Qy    1265 CATGTCCGGGGCAGGGAGCTGA 1286

Db    1200 TATGCCCTCTACAAAGAGCTGA 1221
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RESULT 12
XLU26404
LOCUS       XLU26404     1230 bp    mRNA            VRT       05-JAN-1996
DEFINITION  Xenopus laevis banded hedgehog protein mRNA, complete cds.
ACCESSION   U26404
VERSION     U26404.1  GI:1147831
KEYWORDS    .
SOURCE      African clawed frog.
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
            Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
            Xenopus.
REFERENCE   1  (bases 1 to 1230)
  AUTHORS   Ekker,S.C., McGrew,L.L., Lai,C.J., Lee,J.J., von Kessler,D.P.,
            Moon,R.T. and Beachy,P.A.
  TITLE     Distinct expression and shared activities of members of the
            hedgehog gene family of Xenopus laevis
  JOURNAL   Development 121 (8), 2337-2347 (1995)
  MEDLINE   95401852
REFERENCE   2  (bases 1 to 1230)
  AUTHORS   Ekker,S.C., McGrew,L.L., Lai,C.-J., Lee,J.J., von Kessler,D.P.,
            Moon,R.T. and Beachy,P.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-1995) Stephen C. Ekker, Molecular Biology and
            Genetics, Johns Hopkins University, 725 N. Wolfe St, 714 PCTB,
            Baltimore, MD 21205, USA
FEATURES             Location/Qualifiers
     source          1. .1230
                     /organism="Xenopus laevis"
                     /db_xref="taxon:8355"
     CDS             1. .1230
                     /note="secreted signaling molecule; Method: conceptual
                     translation supplied by author"
                     /codon_start=1
                     /product="banded hedgehog protein"
                     /protein_id="AAA85165.1"
                     /db_xref="GI:1147832"
                     /translation="MQLPKVVLLLCAAALLLSGAVRGCGPGRVVGRRRRPTKLSPLSY
                     KQFSPNVPEKTLGASGRYEGKISRNSERFKELTPNYNPDIIFKDEEITGADRLMTQRC
                     KDRLNSLAISVMNQWPGVKLRVTEGWDEDGHHFEESLHYEGRAVDITTSDRDRNKYGM
                     LARLAVEAGFDWVYYESKAHIHCSVKSEHSAAAKTGGCFPGEALATLESGEKIPVSQL
                     SPGLRVLAMDNSGRPTYSDFLSFLDHSPKEEHMFQVIKTQDPHRRLFLTPAHLIFVSD
                     NYSTPASEFQAVFASSVRPGQYILVSNVVGLIPAKVRSVNTQTNYGAYAPLTQHGTLV
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BASE COUNT      315 a    303 c    335 g    277 t
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Query Match 31.4%; Score 509.6; DB 4; Length 1230;
Best Local Similarity 65.5%; Pred. No. 4e-79;
Matches 781; Conservative 0; Mismatches 399; Indels 12; Gaps 2;

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Qy    104 GCTGCTGGTGGTGCCCGCGGCATGGGGCTGCGGGCCGGGTCGGGTGGTGGGCAGCCGCCG 163
Db     42 GCTGCTCCTGAGCGGGGCGGTGCGGGGTTGCGGACCGGGAAGGGTGGTCGGCAGGAGGCG 101

Qy    164 GCGACCGCCACGCAAACTCGTGCCGCTCGCCTACAAGCAGTTCAGCCCCAATGTGCCCGA 223
Db    102 CAGACCGAC---CAAGCTCAGCCCGCTCTCCTACAAGCAGTTCAGCCCGAATGTACCCGA 158

Qy    224 GAAGACCCTGGGCGCCAGCGGACGCTATGAAGGCAAGATCGCTCGCAGCTCCGAGCGCTT 283
Db    159 GAAGACCCTGGGAGCCAGCGGCAGGTACGAAGGGAAGATCTCCCGCAACTCAGAACGCTT 218

Qy    284 CAAGGAGCTCACCCCCAATTACAATCCAGACATCATCTTCAAGGACGAGGAGAACACAGG 343
Db    219 CAAGGAACTCACCCCCAACTACAACCCGGACATTATATTCAAGGACGAAGAGATCACGGG 278

Qy    344 CGCCGACCGCCTCATGACCCAGCGCTGCAAGGACCGCCTGAACTCGCTGGCTATCTCGGT 403
Db    279 GGCAGACCGGCTCATGACCCAGCGCTGCAAAGACCGACTGAATTCCTTGGCCATTTCTGT 338

Qy    404 GATGAACCAGTGGCCCGGTGTGAAGCTGCGGGTGACCGAGGGCTGGGACGAGGACGGCCA 463
Db    339 CATGAACCAGTGGCCTGGAGTTAAACTGAGAGTGACAGAAGGCTGGGATGAGGATGGACA 398

Qy    464 CCACTCAGAGGAGTCCCTGCATTATGAGGGCCGCGCGGTGGACATCACCACATCAGACCG 523
Db    399 CCATTTCGAAGAATCCTTGCACTACGAGGGGCGTGCAGTCGACATCACCACATCAGACCG 458

Qy    524 CGACCGCAATAAGTATGGACTGCTGGCGCGCTTGGCAGTGGAGGCCGGCTTTGACTGGGT 583
Db    459 GGATCGCAATAAGTACGGAATGCTGGCTAGGCTGGCAGTGGAAGCTGGATTTGACTGGGT 518

Qy    584 GTATTACGAGTCAAAGGCCCACGTGCATTGCTCCGTCAAGTCCGAGCACTCGGCCGCAGC 643
Db    519 CTACTATGAGTCCAAAGCCCATATCCATTGCTCGGTGAAGTCAGAACATTCTGCCGCTGC 578

Qy    644 CAAGACGGGCGGCTGCTTCCCTGCCGGAGCCCAGGTACGCCTGGAGAGTGGGGCGCGTGT 703
Db    579 CAAGACTGGAGGCTGTTTCCCAGGAGAGGCACTGGCCACATTGGAGTCTGGTGAGAAGAT 638

Qy    704 GGCCTTGTCAGCCGTGAGGCCGGGAGACCGTGTGCTGGCCATGGGGGAGGATGGGAGCCC 763
Db    639 ACCAGTTTCTCAGCTGAGCCCAGGCCTACGTGTCCTGGCTATGGACAACAGTGGGAGGCC 698

Qy    764 CACCTTCAGCGATGTGCTCATTTTCCTGGACCGCGAGCCCCACAGGCTGAGAGCCTTCCA 823
Db    699 AACGTACAGTGACTTTTTGAGCTTTTAGATCACAGTCCCAAAGAAGAGCACATGTTCCA 758

Qy    824 GGTCATCGAGACTCAGGACCCCCCACGCCGCCTGGCACTCACACCCGCTCACCTGCTCTT 883
Db    759 GGTTATAAAGACTCAAGACCCACACCGTCGTTTGTTCTTAACACCAGCCCATTTGATCTT 818

Qy    884 TACGGCTGACAATCACACGGAGCCGGCAGCCCGCTTCCGGGCCACATTTGCCAGCCACGT 943
Db    819 TGTTTCGGACAATTATTCCACACCAGCTTCGGAATTCCAGGCAGTATTTGCAAGCAGTGT 878

Qy    944 GCAGCCTGGCCAGTACGTGCTGGTGGCTGGGGTGCCAGGCCTGCAGCCTGCCCGCGTGGC 1003
Db    879 AAGGCCAGGGCAATATATTCTAGTATCAAATGTGGTGGGGCTGATACCTGCTAAAGTAAG 938

Qy   1004 AGCTGTCTCTACACACGTGGCCCTCGGGGCCTACGCCCCGCTCACAAAGCATGGGACACT 1063
Db    939 GTCAGTAAATACGCAGACAAACTATGGGGCTTATGCTCCTCTAACTCAGCATGGGACACT 998

Qy   1064 GGTGGTGGAGGATGTGGTGGCATCCTGCTTCGCGGCCGTGGCTGACCACCACCTGGCTCA 1123
Db     999 CGTGGTAGATGATGTGGTTGTGTCCTGTTTTGCCCTGGTACAGAAACAGAGGCTAGCCCA 1058

Qy   1124 GTTGGCCTTCTGGCCCCTGAGACTCTTTCACAGCT---------TGGCATGGGGCAGCTG 1174
Db    1059 AATTGTTTATTGGCCTCTCCGGGTACTCTACAATTTAGGGATAATAGCAGGAACGCAACC 1118

Qy   1175 GACCCCGGGGGAGGGTGTGCATTGGTACCCCCAGCTGCTCTACCGCCTGGGGCGTCTCCT 1234
Db    1119 ATCACAGCAGATGGGCATTCACTGGTATAGCAAAGCTCTGTATCACTTGGGCAGGCTAAT 1178

Qy   1235 GCTAGAAGAGGGCAGCTTCCACCCACTGGGCATGTCCGGGGCAGGGAGCTGA 1286
Db    1179 ACTTCATGGGAATGAGTTCCATCCTTTAGGAATTGTCCAGTTGGAAAGCTGA 1230
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RESULT 13
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LOCUS       CHKZPAMED    1567 bp    mRNA            VRT       04-OCT-1999
DEFINITION  Gallus gallus sonic hedgehog mRNA, complete cds.
ACCESSION   L28099
VERSION     L28099.1  GI:453526
KEYWORDS    .
SOURCE      chicken.
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
            Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 1567)
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  AUTHORS   Riddle,R.D., Johnson,R.L., Laufer,E. and Tabin,C.
  TITLE     Sonic hedgehog mediates the polarizing activity of the ZPA
  JOURNAL   Cell 75, 1401-1416 (1993)
  MEDLINE   94094333
FEATURES             Location/Qualifiers
     source          1. .1567
                     /organism="Gallus gallus"
                     /db_xref="taxon:9031"
                     /tissue_type="embryo"
                     /dev_stage="stage 20-22"
     CDS             227. .1504
                     /codon_start=1
                     /product="sonic hedgehog"
                     /protein_id="AAA72428.1"
                     /db_xref="GI:453527"
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                     LAYKQFIPNVAEKTLGASGRYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMT
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                     YGMLARLAVEAGFDWVYYESKAHIHCSVKAENSVAAKSGGCFPGSATVHLEHGGTKLV
                     KDLSPGDRVLAADADGRLLYSDFLTFLDRMDSSRKLFYVIETRQPRARLLLTAAHLLF
                     VAPQHNQSEATGSTSGQALFASNVKPGQRVYVLGEGGQQLLPASVHSVSLREEASGAY
                     APLTAQGTILINRVLASCYAVIEEHSWAHWAFAPFRLAQGLLAALCPDGAIPTAATTT
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BASE COUNT      347 a    457 c    475 g    288 t
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  Best Local Similarity   65.2%;  Pred. No. 8.1e-71;
  Matches  766;  Conservative    0;  Mismatches  361;  Indels   48;  Gaps    4;

Qy     163 GGCGACCGCCACGCAAACTCGTGCCGCTCGCCTACAAGCAGTTCAGCCCCAATGTGCCCG 222
           || | |  ||    || ||    ||| | ||||| ||||||| |  |||||||| | |
Db     333 GGAGGCACCCCAAAAAGCTGACCCCGTTAGCCTATAAGCAGTTTATTCCCAATGTGGCAG 392

Qy     223 AGAAGACCCTGGGCGCCAGCGGACGCTATGAAGGCAAGATCGCTCGCAGCTCCGAGCGCT 282
           |||||||||| || ||||| ||| | |||||||| |||||| |  | | ||||||| | |
Db     393 AGAAGACCCTAGGGGCCAGTGGAAGATATGAAGGGAAGATCACAAGAAACTCCGAGAGAT 452

Qy     283 TCAAGGAGCTCACCCCCAATTACAATCCAGACATCATCTTCAAGGACGAGGAGAACACAG 342
           | || || || ||||| |||||||| || ||||| || || ||||| || |||||||| |
Db     453 TTAAAGAACTAACCCCAAATTACAACCCTGACATTATTTTTAAGGATGAAGAGAACACGG 512

Qy     343 GCGCCGACCGCCTCATGACCCAGCGCTGCAAGGACCGCCTGAACTCGCTGGCTATCTCGG 402
           | || ||| | || ||||| ||||||||||||||    |||||  | ||||| |||||||
Db     513 GAGCTGACAGACTGATGACTCAGCGCTGCAAGGACAAGCTGAATGCCCTGGCGATCTCGG 572

Qy     403 TGATGAACCAGTGGCCCGGTGTGAAGCTGCGGGTGACCGAGGGCTGGGACGAGGACGGCC 462
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||| ||||
Db     573 TGATGAACCAGTGGCCCGGGGTGAAGCTGCGGGTGACCGAGGGCTGGGACGAGGATGGCC 632

Qy     463 ACCACTCAGAGGAGTCCCTGCATTATGAGGGCCGCGCGGTGGACATCACCACATCAGACC 522
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Db     633 ATCACTCCGAGGAATCGCTGCACTACGAGGGTCGCGCCGTGGACATCACCACGTCGGATC 692

Qy     523 GCGACCGCAATAAGTATGGACTGCTGGCGCGCTTGGCAGTGGAGGCCGGCTTTGACTGGG 582
           | |||||||  ||||| ||| ||||||| ||| | || || |||||||||| |||||||
Db     693 GGGACCGCAGCAAGTACGGAATGCTGGCCCGCCTCGCCGTCGAGGCCGGCTTCGACTGGG 752

Qy     583 TGTATTACGAGTCAAAGGCCCACGTGCATTGCTCCGTCAAGTCCGAGCACTCGGCCGCAG 642
           | || |||||||| ||||| ||| | || ||||||||||  | ||  |||| |  ||||
Db     753 TCTACTACGAGTCCAAGGCGCACATCCACTGCTCCGTCAAAGCAGAAAACTCAGTGGCAG 812

Qy     643 CCAAGACGGGCGGCTGCTTCCCTGCCGGAGCCCAGGTACGCCTGGAGAGTGGGGCGCGTG 702
           | ||  | || |||||||||||||  |||| || | |||||||  ||| |
Db     813 CGAAATCAGGAGGCTGCTTCCCTGGCTCAGCCACAGTGCACCTGGAGCATGGAGGCACCA 872

Qy     703 TGGCCTTGTCAGCCGTGAGGCCGGGAGACCGTGTGCTGGCCATGGGGGAGGATGGGAGCC 762
           |    ||   | | |||| || || ||||| ||||||||   |  | ||| ||  | |
Db     873 AGCTGGTGAAGGACCTGAGCCCTGGGGACCGCGTGCTGGCTGCTGACGCGGACGGCCGGC 932

Qy     763 CCACCTTCAGCGATGTGCTCATTTTCCTGGACCGCGAGCCCCACAGGCTGAGAGCCTTCC 822
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Db     933 TGCTCTACAGTGACTTCCTCACCTTCCTCGACCGGATGGACAGCTCCCGAAAGCTCTTCT 992

Qy     823 AGGTCATCGAGACTCAGGACCCCCCACGCCGCCTGGCACTCACACCCGCTCACCTGCTCT 882
           | ||||||||||| | | |||||    ||| |||  ||| ||  |  || ||||||||||
Db     993 ACGTCATCGAGACGCGGCAGCCCCGGGCCCGGCTGCTACTGACGGCGGCCCACCTGCTCT 1052

Qy     883 TTACGGCTGACAATCACACGGAGCCGG----------CAGCCCGCTTCCGGGCCACAT 930
           ||  |||   | | ||||   || |||            |  || |   || |||    |
Db    1053 TTGTGGCCCCCCAGCACAACCAGTCGGAGGCCACAGGGTCCACCAGTGGCCAGGCGCTCT 1112

Qy     931 TTGCCAGCCACGTGCAGCCTGGCCA------GTACGTGCTGGTGGCTGGGGTGCCAGGCC 984
           | |||||| ||||| ||||||||||       || |||||||  |  || | ||     |
Db    1113 TCGCCAGCAACGTGAAGCCTGGCCAACGTGTCTATGTGCTGGGCGAGGGCGGGCAGCAGC 1172

Qy     985 TGCAGCCTGCCCGCGTGGCAGCTGTCTCTACAC---ACGTGGCCCTCGGGGCCTACGCCC 1041
           ||| ||| ||    ||       |||||    |  | | |||   ||| ||||||||||
Db    1173 TGCTGCCGGCGTCTGTCCACAGCGTCTCATTGCGGGAGGAGGCGTCCGGAGCCTACGCCC 1232

Qy    1042 CGCTCACAAAGCATGGGACACTGGTGGTGGAGGATGTGGTGGCATCCTGCTTCGCGGCCG 1101
           | |||||    || || ||  |  |  |  |    ||| |||| ||||||| ||| | |
Db    1233 CACTCACCGCCCAGGGCACCATCCTCATCAACCGGGTGTTGGCCTCCTGCTACGCCGTCA 1292

Qy    1102 TGGCTGACCACCACCTGGCTCAGTTGGCCTTCTGGCCCCTGAGACTCTTTCACAGCTTGG 1161
           | |  || |||     ||| || | |||||||  ||  |  |  |   |||  |  ||
Db    1293 TCGAGGAGCACAGTTGGGCCCATTGGGCCTTCGCACCATTCCGCTTGGCTCAGGGGCTGC 1352

Qy    1162 CATGGGGCAGCTGGACCCCGGGGGAG-------------------------GGTGTGC 1194
               | |  |||  |   ||||                            ||  | |
Db    1353 TGGCCGCCCTCTGCCCAGATGGGGCCATCCCTACTGCCGCCACCACCACCACTGGCATCC 1412

Qy    1195 ATTGGTACCCCCAGCTGCTCTACCGCCTGGGGCGTCTCCTGCTAGAAGAGGGCAGCTTCC 1254
           |||||||| | | ||| |||||||| | ||  |     |||| || |  | |    | |
Db    1413 ATTGGTACTCACGGCTCCTCTACCGCATCGGCAGCTGGGTGCTGGATGGTGACGCGCTGC 1472

Qy    1255 ACCCACTGGGCATGTCCGGGGCAGGGAGCTGAAAG 1289
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Db    1473 ATCCGCTGGGCATGGTGGCACCGGCCAGCTGAGAG 1507
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RESULT  14
AR021198
LOCUS       AR021198     1277 bp    DNA             PAT       05-DEC-1998
DEFINITION  Sequence 1 from patent US 5789543.
ACCESSION   AR021198
VERSION     AR021198.1  GI:3975813
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1277)
  AUTHORS   Ingham,P.W., McMahon,A.P. and Tabin,C.J.
  TITLE     Vertebrate embryonic pattern-inducing proteins and uses related
            thereto
  JOURNAL   Patent: US 5789543-A 1 04-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .1277
                     /organism="unknown"
BASE COUNT      262 a    396 c    387 g    232 t
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  Best Local Similarity   65.2%;  Pred. No. 2.2e-70;
  Matches  763;  Conservative    0;  Mismatches  360;  Indels   48;  Gaps    4;

Qy     163 GGCGACCGCCACGCAAACTCGTGCCGCTCGCCTACAAGCAGTTCAGCCCCAATGTGCCCG 222
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Db     107 GGAGGCACCCCAAAAAGCTGACCCCGTTAGCCTATAAGCAGTTTATTCCCAATGTGGCAG 166

Qy     223 AGAAGACCCTGGGCGCCAGCGGACGCTATGAAGGCAAGATCGCTCGCAGCTCCGAGCGCT 282
           |||||||||| || ||||| ||| | |||||||| |||||| |  | | ||||||| | |
Db     167 AGAAGACCCTAGGGGCCAGTGGAAGATATGAAGGGAAGATCACAAGAAACTCCGAGAGAT 226
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Qy    283 TCAAGGAGCTCACCCCCAATTACAATCCAGACATCATCTTCAAGGACGAGGAGAACACAG 342
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Db    227 TTAAAGAACTAACCCCAAATTACAACCCTGACATTATTTTTAAGGATGAAGAGAACACGG 286

Qy    343 GCGCCGACCGCCTCATGACCCAGCGCTGCAAGGACCGCCTGAACTCGCTGGCTATCTCGG 402
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Db    287 GAGCTGACAGACTGATGACTCAGCGCTGCAAGGACAAGCTGAATGCCCTGGCGATCTCGG 346

Qy    403 TGATGAACCAGTGGCCCGGTGTGAAGCTGCGGGTGACCGAGGGCTGGGACGAGGACGGCC 462
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Db    347 TGATGAACCAGTGGCCCGGGGTGAAGCTGCGGGTGACCGAGGGCTGGGACGAGGATGGCC 406

Qy    463 ACCACTCAGAGGAGTCCCTGCATTATGAGGGCCGCGCGGTGGACATCACCACATCAGACC 522
          | ||||| ||||| || ||||| || ||||| ||||| |||||||||||||| || || |
Db    407 ATCACTCCGAGGAATCGCTGCACTACGAGGGTCGCGCCGTGGACATCACCACGTCGGATC 466

Qy    523 GCGACCGCAATAAGTATGGACTGCTGGCGCGCTTGGCAGTGGAGGCCGGCTTTGACTGGG 582
          | ||||||| ||||| ||| ||||||| ||| | || || |||||||||||| |||||||
Db    467 GGGACCGCAGCAAGTACGGAATGCTGGCCCGCCTCGCCGTCGAGGCCGGCTTCGACTGGG 526

Qy    583 TGTATTACGAGTCAAAGGCCCACGTGCATTGCTCCGTCAAGTCCGAGCACTCGGCCGCAG 642
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Db    527 TCTACTACGAGTCCAAGGCGCACATCCACTGCTCCGTCAAAGCAGAAAACTCAGTGGCAG 586

Qy    643 CCAAGACGGGCGGCTGCTTCCCTGCCGGAGCCCAGGTACGCCTGGAGAGTGGGGCGCGTG 702
          | ||  | || ||||||||||||| |  ||||   || | |||||||  ||| |
Db    587 CGAAATCAGGAGGCTGCTTCCCTGGCTCAGCCACAGTGCACCTGGAGCATGGAGGCACCA 646

Qy    703 TGGCCTTGTCAGCCGTGAGGCCGGGAGACCGTGTGCTGGCCATGGGGGAGGATGGGAGCC 762
            |    ||   | | |||| || || ||||| |||||||    |  | ||| ||  | |
Db    647 AGCTGGTGAAGGACCTGAGCCCTGGGGACCGCGTGCTGGCTGCTGACGCGGACGGCCGGC 706

Qy    763 CCACCTTCAGCGATGTGCTCATTTTCCTGGACCGCGAGCCCCACAGGCTGAGAGCCTTCC 822
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Db    707 TGCTCTACAGTGACTTCCTCACCTTCCTCGACCGGATGGACAGCTCCCGAAAGCTCTTCT 766

Qy    823 AGGTCATCGAGACTCAGGACCCCCCACGCCGCCTGGCACTCACACCCGCTCACCTGCTCT 882
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Db    767 ACGTCATCGAGACGCGGCAGCCCCGGGCCCGGCTGCTACTGACGGCGGCCCACCTGCTCT 826

Qy    883 TTACGGCTGACAATCACACGGAGCCGG------------CAGCCCGCTTCCGGGCCACAT 930
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Db    827 TTGTGGCCCCCCAGCACAACCAGTCGGAGGCCACAGGGTCCACCAGTGGCCAGGCGCTCT 886

Qy    931 TTGCCAGCCACGTGCAGCCTGGCCA------GTACGTGCTGGTGGCTGGGGTGCCAGGCC 984
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Db    887 TCGCCAGCAACGTGAAGCCTGGCCAACGTGTCTATGTGCTGGGCGAGGGCGGGCAGCAGC 946

Qy    985 TGCAGCCTGCCCGCGTGGCAGCTGTCTCTACAC---ACGTGGCCCTCGGGGCCTACGCCC 1041
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Db    947 TGCTGCCGGCGTCTGTCCACAGCGTCTCATTGCGGGAGGAGGCGTCCGGAGCCTACGCCC 1006

Qy   1042 CGCTCACAAAGCATGGGACACTGGTGGTGGAGGATGTGGTGGCATCCTGCTTCGCGGCCG 1101
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Qy   1102 TGGCTGACCACCACCTGGCTCAGTTGGCCTTCTGGCCCCTGAGACTCTTTCACAGCTTGG 1161
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Db   1067 TCGAGGAGCACAGTTGGGCCCATTGGGCCTTCGCACCATTCCGCTTGGCTCAGGGGCTGC 1126

Qy   1162 CATGGGGCAGCTGGACCCCGGGGGAG-------------------------GGTGTGC 1194
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Db   1127 TGGCCGCCCTCTGCCCAGATGGGGCCATCCCTACTGCCGCCACCACCACCACTGGCATCC 1186

Qy   1195 ATTGGTACCCCCAGCTGCTCTACCGCCTGGGGCGTCTCCTGCTAGAAGAGGGCAGCTTCC 1254
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Db   1187 ATTGGTACTCACGGCTCCTCTACCGCATCGGCAGCTGGGTGCTGGATGGTGACGCGCTGC 1246

Qy   1255 ACCCACTGGGCATGTCCGGGGCAGGGAGCTG 1285
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RESULT  15
AR063080
LOCUS       AR063080     1277 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 1 from patent US 5844079.
ACCESSION   AR063080
VERSION     AR063080.1  GI:5990771
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1277)
  AUTHORS   Ingham,P.W., McMahon,A.P. and Tabin,C.J.
  TITLE     Vertebrate embryonic pattern-inducing proteins, and uses related
            thereto
  JOURNAL   Patent: US 5844079-A 1 01-DEC-1998;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
BASE COUNT      262 a    396 c    387 g    232 t
ORIGIN
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  Query Match             28.3%;  Score 459;  DB 5;  Length 1277;
  Best Local Similarity   65.2%;  Pred. No. 2.2e-70;
  Matches  763;  Conservative    0;  Mismatches  360;  Indels   48;  Gaps    4;

Qy    163 GGCGACCGCCACGCAAACTCGTGCCGCTCGCCTACAAGCAGTTCAGCCCCAATGTGCCCG 222
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Db    107 GGAGGCACCCCAAAAAGCTGACCCCGTTAGCCTATAAGCAGTTTATTCCCAATGTGGCAG 166

Qy    223 AGAAGACCCTGGGCGCCAGCGGACGCTATGAAGGCAAGATCGCTCGCAGCTCCGAGCGCT 282
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Db    167 AGAAGACCCTAGGGGCCAGTGGAAGATATGAAGGGAAGATCACAAGAAACTCCGAGAGAT 226

Qy    283 TCAAGGAGCTCACCCCCAATTACAATCCAGACATCATCTTCAAGGACGAGGAGAACACAG 342
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Db    227 TTAAAGAACTAACCCCAAATTACAACCCTGACATTATTTTTAAGGATGAAGAGAACACGG 286

Qy    343 GCGCCGACCGCCTCATGACCCAGCGCTGCAAGGACCGCCTGAACTCGCTGGCTATCTCGG 402
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Db    287 GAGCTGACAGACTGATGACTCAGCGCTGCAAGGACAAGCTGAATGCCCTGGCGATCTCGG 346

Qy    403 TGATGAACCAGTGGCCCGGTGTGAAGCTGCGGGTGACCGAGGGCTGGGACGAGGACGGCC 462
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||| ||||
Db    347 TGATGAACCAGTGGCCCGGGGTGAAGCTGCGGGTGACCGAGGGCTGGGACGAGGATGGCC 406

Qy    463 ACCACTCAGAGGAGTCCCTGCATTATGAGGGCCGCGCGGTGGACATCACCACATCAGACC 522
          | ||||| ||||| || ||||| || ||||| ||||| |||||||||||||| || || |
Db    407 ATCACTCCGAGGAATCGCTGCACTACGAGGGTCGCGCCGTGGACATCACCACGTCGGATC 466

Qy    523 GCGACCGCAATAAGTATGGACTGCTGGCGCGCTTGGCAGTGGAGGCCGGCTTTGACTGGG 582
          | ||||||| ||||| ||| ||||||| ||| | || || |||||||||||| |||||||
Db    467 GGGACCGCAGCAAGTACGGAATGCTGGCCCGCCTCGCCGTCGAGGCCGGCTTCGACTGGG 526

Qy    583 TGTATTACGAGTCAAAGGCCCACGTGCATTGCTCCGTCAAGTCCGAGCACTCGGCCGCAG 642
          | || ||||||| ||||| ||| | || ||||||||||  | ||  |||| |  ||||
Db    527 TCTACTACGAGTCCAAGGCGCACATCCACTGCTCCGTCAAAGCAGAAAACTCAGTGGCAG 586

Qy    643 CCAAGACGGGCGGCTGCTTCCCTGCCGGAGCCCAGGTACGCCTGGAGAGTGGGGCGCGTG 702
          | ||  | || ||||||||||||| |  ||||   || | |||||||  ||| |
Db    587 CGAAATCAGGAGGCTGCTTCCCTGGCTCAGCCACAGTGCACCTGGAGCATGGAGGCACCA 646

Qy    703 TGGCCTTGTCAGCCGTGAGGCCGGGAGACCGTGTGCTGGCCATGGGGGAGGATGGGAGCC 762
            |    ||   | | |||| || || ||||| |||||||    |  | ||| ||  | |
Db    647 AGCTGGTGAAGGACCTGAGCCCTGGGGACCGCGTGCTGGCTGCTGACGCGGACGGCCGGC 706

Qy    763 CCACCTTCAGCGATGTGCTCATTTTCCTGGACCGCGAGCCCCACAGGCTGAGAGCCTTCC 822
              || ||| ||  | ||||  ||||| |||||   |  |  |   |  |    ||||
Db    707 TGCTCTACAGTGACTTCCTCACCTTCCTCGACCGGATGGACAGCTCCCGAAAGCTCTTCT 766

Qy    823 AGGTCATCGAGACTCAGGACCCCCCACGCCGCCTGGCACTCACACCCGCTCACCTGCTCT 882
          | ||||||||||| | | | ||||    ||| |||  ||| ||  | || ||||||||||
Db    767 ACGTCATCGAGACGCGGCAGCCCCGGGCCCGGCTGCTACTGACGGCGGCCCACCTGCTCT 826
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Qy    883 TTACGGCTGACAATCACACGGAGCCGG-----------CAGCCCGCTTCCGGGCCACAT 930
          ||  |||   | | ||||   || |||            |  || |   || |||    |
Db    827 TTGTGGCCCCCCAGCACAACCAGTCGGAGGCCACAGGGTCCACCAGTGGCCAGGCGCTCT 886

Qy    931 TTGCCAGCCACGTGCAGCCTGGCCA------GTACGTGCTGGTGGCTGGGGTGCCAGGCC 984
          | |||||| ||||| ||||||||||       || |||||||  |  || | ||     |
Db    887 TCGCCAGCAACGTGAAGCCTGGCCAACGTGTCTATGTGCTGGGCGAGGGCGGGCAGCAGC 946

Qy    985 TGCAGCCTGCCCGCGTGGCAGCTGTCTCTACAC---ACGTGGCCCTCGGGGCCTACGCCC 1041
          ||| ||| ||    ||       |||||    |   | | |||   ||| ||||||||||
Db    947 TGCTGCCGGCGTCTGTCCACAGCGTCTCATTGCGGGAGGAGGCGTCCGGAGCCTACGCCC 1006

Qy   1042 CGCTCACAAAGCATGGGACACTGGTGGTGGAGGATGTGGTGGCATCCTGCTTCGCGGCCG 1101
          | |||||    || || ||  |  |  |  |    ||| |||| ||||||| ||| | |
Db   1007 CACTCACCGCCCAGGGCACCATCCTCATCAACCGGGTGTTGGCCTCCTGCTACGCCGTCA 1066

Qy   1102 TGGCTGACCACCACCTGGCTCAGTTGGCCTTCTGGCCCCTGAGACTCTTTCACAGCTTGG 1161
          | |  || |||     ||| || | |||||||   ||  |  |  |   |||  |  ||
Db   1067 TCGAGGAGCACAGTTGGGCCCATTGGGCCTTCGCACCATTCCGCTTGGCTCAGGGGCTGC 1126

Qy   1162 CATGGGGCAGCTGGACCCCGGGGGAG--------------------------GGTGTGC 1194
             | |  |||  |    ||||                              ||  | |
Db   1127 TGGCCGCCCTCTGCCCAGATGGGGCCATCCCTACTGCCGCCACCACCACCACTGGCATCC 1186

Qy   1195 ATTGGTACCCCCAGCTGCTCTACCGCCTGGGGCGTCTCCTGCTAGAAGAGGGCAGCTTCC 1254
          |||||||| | | ||| |||||||||| | ||  |     |||| || |  | |    | |
Db   1187 ATTGGTACTCACGGCTCCTCTACCGCATCGGCAGCTGGGTGCTGGATGGTGACGCGCTGC 1246

Qy   1255 ACCCACTGGGCATGTCCGGGGCAGGGAGCTG 1285
          | || |||||||||   |   | |  |||||
Db   1247 ATCCGCTGGGCATGGTGGCACCGGCCAGCTG 1277
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